



CC alpha helix at the C-terminal end of the gp41 ectodomain, and complexes with DP-107 (correspond to amino acids 558-595), which contains a leucine zipper motif. The peptides complex via non-covalent protein-protein interactions, and possess anti-viral activity. Homologues of these peptides were identified by a computer assisted peptide sequence search. The peptides inhibit transmission to uninfected cells, and can also be used as type and/or subtype specific diagnostic tools. (Updated on 25-MAR-2003 to correct PN field.)

XX sequence 36 AA;

Query Match 100.0%; Score 195; DB 2; Length 36; Best Local Similarity 100.0%; Pred. No. 8.8e-17; Matches 36; Conservat. 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLILHSILSERSONQQEKENQOBELLDKMASLWNWF 36  
Db 1 YTSLILHSILSERSONQQEKENQOBELLDKMASLWNWF 36

RESULT 2  
AAR98398  
XX  
AC AAR98398;  
XX  
DT 16-OCT-2003 (revised)  
XX  
DT 17-FEB-1997 (first entry)

DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.  
KW Antifusogenic activity; antiviral capability; coiled-coil peptide;  
KW ALIMOTIS; 107x178x4; PLZP search motif; viral transmission; HIV;  
KW influenza virus; hepatitis B virus.  
OS Human immunodeficiency virus 1.

XX WO9619495-A1.  
PN  
XX  
PD 27-JUN-1996.  
XX  
PF 20-DEC-1995; 95WO-US016733.  
XX  
PR 20-DEC-1994; 94US-00360107.  
PR 06-JUN-1995; 95US-00470896.  
XX  
PA (UYDU-) UNIV DUKE.  
PA (TRIM-) TRIMERIS INC.  
XX  
PR 1997-099886/09.  
XX  
PT Compens. contg. DP-178 or DP-107 in combination with other therapeutic agent useful for treatment of HIV infection, esp. by inhibiting replication or transmission of HIV.  
XX  
PS Claim 2; Fig 1; 84pp; English.

XX AAW17011 represents a peptide designated DP-178, a peptide derived from HIV type 1 glycoprotein 41(gp41) transmembrane protein. The peptide corresponds to residues 638-673 of gp41. DP-178 and its derivatives are used in combination with a therapeutic agent, e.g. a reverse transcriptase, viral protease, cytokine, glycosylation or viral mRNA processing inhibitor or a nucleoside inhibitor. The peptides work by inhibiting viral replication or inhibiting transmission. They may also be used in vaccines for protecting against HIV infection. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 36 AA;  
Query Match 100.0%; Score 195; DB 2; Length 36; Best Local Similarity 100.0%; Pred. No. 8.8e-17; Matches 36; Conservat. 0; Mismatches 0; Indels 0; Gaps 0;  
PS Disclosure; Fig 1; 471pp; English.  
XX  
CC The sequences given in AAR98398-408 represent peptides which exhibit anti-sensegenic activity, anti-viral capability and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. These peptides are recognised by the ALIMOTIS, 107x178x4 and PLZP search motifs. These peptides may be used to inhibit the transmission of a virus, pref. HIV, influenza virus, or hepatitis B virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)  
XX Sequence 36 AA;

Query Match 100.0%; Score 195; DB 2; Length 36; Best Local Similarity 100.0%; Pred. No. 8.8e-17; Matches 36; Conservat. 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLILHSILSERSONQQEKENQOBELLDKMASLWNWF 36  
Db 1 YTSLILHSILSERSONQQEKENQOBELLDKMASLWNWF 36

RESULT 4  
AAY22912  
ID AAY22912 Standard; peptide; 36 AA.  
AC AAY22912;  
XX  
DT 19-AUG-1999 (first entry)

DB SEQ ID NO. 108 from WO9820036.



KW T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN W09948513-A1.  
 XX  
 PD 30-SEP-1999.  
 XX  
 PR 22-MAR-1999; 99WO-US006230.  
 XX  
 PR 23-MAR-1998; 98US-00045920.  
 XX  
 PR 01-MAY-1998; 98US-00071877.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 XX  
 PT Kang M., Bray B., Lichty M., Mader C., Merutka G;  
 XX  
 DR WPI; 1999-591038/50.  
 XX  
 PA Methods of peptide synthesis, particularly used to produce T-20 or T-20  
 PT like peptides.  
 XX  
 PS Disclosure; Page 9; 120pp; English.  
 XX  
 The present sequence represents a peptide, designated T-20 (or DP-178),  
 CC that corresponds to amino acids 638-673 of the transmembrane protein gp41  
 CC of HIV-1 LAI isolate. The invention relates to methods for the synthesis  
 CC of peptides, in particular C- and N-terminal modified T-20 (see AAY31955)  
 CC and T-20-like peptides. The method involves synthesizing specific side-  
 CC chain protected peptide fragment intermediates (see AAY31956-73) of T-20  
 CC or a T-20-like peptide on a solid support, coupling the protected  
 CC fragments in solution to form a protected T-20 or T-20-like peptide,  
 CC followed by deprotection of the side chains to yield the final T-20 or T-  
 CC 20-like peptide. The invention also relates to individual peptide  
 CC fragments which act as intermediates in the synthesis of peptides of  
 CC interest (e.g. T-20), and to particular groups of peptide fragments which  
 CC act as intermediates in the synthesis of the peptide of interest. The  
 CC method allows for the large scale, economical production of high purity  
 CC peptides. (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SQ sequence 36 AA;  
 Query Match 100.0%; Score 195; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSILHSLIESQNQEKNEQBLLDKRASLWNWF 36  
 Db 1 YTSILHSLIESQNQEKNEQBLLDKRASLWNWF 36  
 RESULT 7  
 AAY31955  
 ID AAY31955 standard; peptide; 36 AA.  
 Db 1 YTSILHSLIESQNQEKNEQBLLDKRASLWNWF 36  
 RESULT 8  
 AAY89999  
 ID AAY89999 standard; peptide; 36 AA.  
 AC AAY89999;  
 XX  
 DT 23-MAY-2000 (first entry)  
 DE Core polypeptide fragment T No. 1598.  
 XX  
 Core polypeptide fragment T No. 1598.  
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN W09959615-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PR 20-MAY-1999; 99WO-US011219.  
 XX  
 PR 20-MAY-1998; 98US-00082279.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 XX  
 PI Barney S., Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PN W09948513-A1.

WPI: 2000-136792/12. DR  
 XX PT  
 XX PT comprises enhancer sequence.  
 XX PS Disclosure; Page 48; 124pp; English.  
 XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are biactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor, hormone or angiogenic  
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic  
 CC factor. The peptides of the invention can be used for inhibiting viral  
 CC infection and can be used in anti-viral and anti-fusogenic treatments.  
 CC Sequences AAY8651-Y9055 represent core polypeptide fragments that can  
 CC be used in the invention. Some sequences among those indicated also  
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
 XX SQ Sequence 36 AA;  
 XX  
 Query Match 100.0%; Score 195; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17; Matches 36; Conservative 0; Mismatches 0; Indels 0; Caps 0  
 QY 1 YTSIHLISLIESQNOQEKGQFQELLDKWAISLWNWF 36  
 Db 1 YTSIHLISLIESQNOQEKGQFQELLDKWAISLWNWF 36  
 XX  
 RESULT 9  
 AAY8665  
 ID AAY8665 standard; peptide; 36 AA.  
 XX  
 AC AAY8665;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX DE Core polypeptide fragment T No. 20.  
 XX  
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 XX OS Unidentified.  
 XX PN W09959615-A1.  
 XX  
 PD 25-NOV-1999.  
 XX PF 20-MAY-1999; 99WO-US011219.  
 XX PR 20-MAY-1998; 98US-00082279.  
 XX PA (TRIM-) TRIMERIS INC.  
 XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX DR WPI; 2000-136792/12.  
 XX PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 XX comprises enhancer sequence.  
 XX Disclosure; Page 21; 124pp; English.  
 XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide

CC interleukin, interferon, colony stimulating factor, hormone or angiogenic  
 CC factor. The peptides of the invention can be used for inhibiting viral  
 CC infection and can be used in anti-viral and anti-fusogenic treatments.  
 CC Sequences AY8651-Y90055 represent core polypeptide fragments that can  
 CC be used in the invention. Some sequences among those indicated also  
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
 XX sequence 36 AA;

Query Match 100.0%; Score 195; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17; Mismatches 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSЛИHSLIERSQNQEKNEQELLDKWAШLWWF 36  
 Db 1 YTSЛИHSLIERSQNQEKNEQELLDKWAШLWWF 36

RESULT 11

AY8982 AAY8982 standard; peptide; 36 AA.

XX

Qy 1 YTSЛИHSLIERSQNQEKNEQELLDKWAШLWWF 36  
 Db 1 YTSЛИHSLIERSQNQEKNEQELLDKWAШLWWF 36

Core polypeptide fragment T No. 1559.

XX

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 anti-fusogenic; differentiation factor; interleukin; interferon;  
 colony stimulating factor; hormone; angiogenic factor.

XX

AC AAY8982;

XX

DT 23-MAY-2000 (first entry)

XX

AY8982 AAY8982 standard; peptide; 36 AA.

XX

AC AAY8982;

XX

DT 23-MAY-2000 (first entry)

XX

DB Core polypeptide fragment T No. 974.

XX

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 anti-fusogenic; differentiation factor; interleukin; interferon;  
 colony stimulating factor; hormone; angiogenic factor.

XX

OS Unidentified.

XX

DT 23-MAY-2000 (first entry)

XX

DB Core polypeptide fragment T No. 974.

XX

W0959615-A1.

XX

PD 25-NOV-1999.

XX

PN 99WO-US011219.

XX

PF 20-MAY-1998; 98US-00082279.

XX

PR 20-MAY-1998; 98US-00082279.

XX

PA (TRIM-) TRIMERIS INC.

XX

PA (TRIM-) TRIMERIS INC.

XX

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX

DR WPI: 2000-136792/12.

XX

PT A new hybrid polypeptide with enhanced pharmacokinetic properties

PT comprises enhancer sequence.

XX

PS Disclosure; Page 36; 124pp; English.

XX

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX

DR WPI: 2000-136792/12.

XX

PT A new hybrid polypeptide with enhanced pharmacokinetic properties

PT comprises enhancer sequence.

XX

PS Disclosure; Page 36; 124pp; English.

XX

PI The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic  
 CC factor. The peptides of the invention can be used for inhibiting viral  
 CC infection and can be used in anti-viral and anti-fusogenic treatments.  
 CC Sequences AY8651-Y90055 represent core polypeptide fragments that can  
 CC be used in the invention. Some sequences among those indicated also  
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
 XX sequence 36 AA;

Query Match 100.0%; Score 195; DB 3; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17; Mismatches 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSЛИHSLIERSQNQEKNEQELLDKWAШLWWF 36  
 Db 1 YTSЛИHSLIERSQNQEKNEQELLDKWAШLWWF 36

RESULT 13  
 AAV89692  
 ID AAV89692 standard; peptide; 36 AA.  
 XX  
 AC AAV89692;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Core polypeptide fragment T No. 1254.  
 XX  
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 anti-fusogenic; differentiation factor; interleukin; interferon;  
 colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN W09959615-A1.  
 XX  
 PR 25-NOV-1999;  
 XX  
 PF 99WO-US011219.  
 XX  
 PR 20-MAY-1999;  
 XX  
 PR 20-MAY-1998; 98US-00082279.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 XX  
 PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 DR WPI; 2000-136792/12.  
 XX  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence.  
 XX  
 PS Disclosure; Page 42; 124pp; English.  
 XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 PT especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that may be introduced into a living system and that can  
 PS function as a pharmacologically useful peptide for the treatment or  
 XX prevention of a disease. The core polypeptides are any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic  
 CC factor. The peptides of the invention can be used for inhibiting viral  
 CC infection and can be used in anti-viral and anti-fusogenic treatments.  
 CC Sequences AAV88651-Y90055 represent core polypeptide fragments that can  
 CC be used in the invention. Some sequences among those indicated also  
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
 XX Sequence 36 AA;  
 SQ

Query Match 100.0%; Score 195; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHSLIESONQEQERNEQELLDKWAISLWNWF 36  
 DB 1 YTSLIHSLIESONQEQERNEQELLDKWAISLWNWF 36

RESULT 14  
 AAV89242  
 ID AAV89242 standard; peptide; 36 AA.  
 XX  
 AC AAV89242;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Core polypeptide fragment T No. 1563.  
 XX  
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 anti-fusogenic; differentiation factor; interleukin; interferon;  
 colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN W09959615-A1.

RESULT 15  
 AAV89983  
 ID AAV89983 standard; peptide; 36 AA.  
 XX  
 AC AAV89983;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Core polypeptide fragment T No. 1563.  
 XX  
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 anti-fusogenic; differentiation factor; interleukin; interferon;  
 colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN W09959615-A1.

XX  
 XX 25-NOV-1999.  
 PD  
 XX  
 PP 20-MAY-1999; 99WO-US011219.  
 PR XX 20-MAY-1999; 98US-00082279.  
 PA XX (TRIM-) TRIMERTS INC.  
 PT Barney S, Guthrie KR, Merutka G, Anwer MK, Lambert DM;  
 DR XX WPI; 2000-13679/12.  
 XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence.  
 XX  
 PS Disclosure; Page 48; 124pp; English.  
 XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are biactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic  
 CC factor. The peptides of the invention can be used for inhibiting viral  
 CC infection and can be used in anti-viral and anti-fusogenic treatments.  
 CC Sequences AY8851-Y0055 represent core polypeptide fragments that can  
 CC be used in the invention. Some sequences among those indicated also  
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
 XX  
 SQ Sequence 35 AA;

Query Match 100.0%; Score 195; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	YSLIHSIESTEQNQEQNEQLELDKWAQWNWF	36
Db	1	YSLIHSIESTEQNQEQNEQLELDKWAQWNWF	36

Search completed: September 20, 2005, 19:44:44  
 Job time : 169 secs

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Om protein - protein search, using SW model

Run on: September 20, 2005, 19:36:25 ; Search time 39 Seconds

(without alignments)  
88.815 Million cell updates/sec

Title: US-09-809-060A-1

Perfect score: 1 YTSLHSLIESQESQNEQELLDKWAQSLWNWF 36

Sequence: S21990

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	195	100.0	851	2 S33985	env polyprotein -
2	195	100.0	854	2 S13288	env protein - huma
3	195	100.0	856	1 VCLJH3	env polyprotein pr
4	195	100.0	861	1 VCLJH3	env polyprotein pr
5	186	95.4	443	2 C41621	env polyprotein P
6	186	95.4	856	1 VCLJ3W	env polyprotein pr
7	186	95.4	856	1 VCLJW	env polyprotein pr
8	186	95.4	861	1 VCLJSC	env polyprotein pr
9	183	93.8	357	2 S21994	env polyprotein pr
10	183	93.8	358	2 S21998	env protein 348, 69-73, 1990
11	182	93.3	357	2 S21996	env protein - human immunodeficiency virus type 1, HIV-1
12	179	91.8	847	2 T09448	C-Species: human immunodeficiency virus type 1, HIV-1
13	179	91.8	847	2 S13289	C-Date: 19-Mar-1997 #Sequence_revision 19-Mar-1997 #Text_change 09-Jul-2004
14	178	91.3	445	2 A41621	C-Accession: S13288
15	177	90.8	358	2 S70417	R-O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
16	177	90.8	358	2 S22000	A-Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c
17	177	90.8	358	2 S22002	A-Reference number: S13288; MUID:91043044; PMID:2172833
18	177	90.8	852	2 T01216	A-Accession: S13288
19	177	90.8	859	1 VCLJMN	A-Status: preliminary
20	176	90.3	357	2 S22004	A-Molecule type: DNA
21	176	90.3	855	1 VCLJAV	A-Residues: 1-851 <CAP>
22	174	89.2	853	2 S554384	A-Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:090178; UNIPROT:078243; UNIP
23	174	89.2	855	1 VCLJZR	C-Superfamily: type E retrovirus env polyprotein
24	173	88.7	357	2 S22006	Query Match 100.0%; Score 95; DB 2; Length 854;
25	173	88.7	843	1 H44001	Best Local Similarity 100.0%; Pred. No. 2, 3e-15; Mismatches 0; Indels 0; Gaps 0;
26	172	88.2	846	1 VCLJND	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
27	170	87.2	357	2 S21992	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
28	170	87.2	852	1 VCLJXK	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
29	86.2	86.2	851	1 VCLJKB	env polyprotein pr

Result No.	Score	Query Match	Length	DB ID	Description
1	195	100.0	851	2 S33985	env polyprotein -
2	195	100.0	854	2 S13288	env protein - huma
3	195	100.0	856	1 VCLJH3	env polyprotein pr
4	195	100.0	861	1 VCLJH3	env polyprotein pr
5	186	95.4	443	2 C41621	env polyprotein P
6	186	95.4	856	1 VCLJ3W	env polyprotein pr
7	186	95.4	856	1 VCLJW	env polyprotein pr
8	186	95.4	861	1 VCLJSC	env polyprotein pr
9	183	93.8	357	2 S21994	env polyprotein pr
10	183	93.8	358	2 S21998	env protein 348, 69-73, 1990
11	182	93.3	357	2 S21996	env protein - human immunodeficiency virus type 1, HIV-1
12	179	91.8	847	2 T09448	C-Species: human immunodeficiency virus type 1, HIV-1
13	179	91.8	847	2 S13289	C-Date: 19-Mar-1997 #Sequence_revision 19-Mar-1997 #Text_change 09-Jul-2004
14	178	91.3	445	2 A41621	C-Accession: S13288
15	177	90.8	358	2 S70417	A-Status: preliminary
16	177	90.8	358	2 S22000	A-Molecule type: DNA
17	177	90.8	358	2 S22002	A-Residues: 1-854 <CAP>
18	177	90.8	852	2 T01216	A-Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:090178; UNIPROT:078243; UNIP
19	177	90.8	859	1 VCLJMN	C-Superfamily: type E retrovirus env polyprotein
20	176	90.3	357	2 S22004	Query Match 100.0%; Score 95; DB 2; Length 854;
21	176	90.3	855	1 VCLJAV	Best Local Similarity 100.0%; Pred. No. 2, 3e-15; Mismatches 0; Indels 0; Gaps 0;
22	174	89.2	853	2 S554384	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
23	174	89.2	855	1 VCLJZR	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
24	173	88.7	357	2 S22006	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
25	173	88.7	843	1 H44001	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
26	172	88.2	846	1 VCLJND	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
27	170	87.2	357	2 S21992	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
28	170	87.2	852	1 VCLJXK	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
29	86.2	86.2	851	1 VCLJKB	env polyprotein pr

VCLJH3

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)

N;Alternate names: coat polyprotein

N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004

C;Accession: A03973

R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora

Ritter, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A;Reference number: A93353; MUID:85111123; PMID:2578615

A;Accession: A03973

A;Molecule type: DNA

A;Residues: 1-856 &lt;RAT&gt;

A;Cross-references: UNIPROT:P03375; GB:ML5654; GB:K02008; GB:K02009; GB:K02010; NID:9326

A;Genetics:

A;Gene: env

C;Superfamily: type E retrovirus env polyprotein

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F;1-3/Domain: signal sequence #status predicted &lt;SIG&gt;

F;31-856/Product: exterior membrane glycoprotein #status predicted &lt;EXT&gt;

F;88-136-141,155-160-186-197-230,234-241-262-276-289,295,301-332,339-356,386,392,397,406

F;611-616,625-637,674-750-816/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 100.0%; Score 195; DB 1; Length 856;

Best Local Similarity 100.0%; Pred. No. 2; 3e-15; Mismatches 0; Indels 0; Gaps 0;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSILHSLIESONQOKEQELLELDKWAQWNWF 36

Db 638 YTSILHSLIESONQOKEQELLELDKWAQWNWF 673

RESULT 4

VCLJIV

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)

N;Alternate names: coat polyprotein virus type 1, HIV-1

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004

C;Accession: A03975

R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.

Cell 40, 9-17, 1985

A;Title: Nucleotide sequence of the AIDS virus, LAV.

A;Reference number: A90866; MUID:85099333; PMID:2981635

A;Accession: A03975

A;Molecule type: DNA

A;Residues: 1-861 &lt;WAT&gt;

A;Cross-references: UNIPROT:P03377; GB:K02013; NID:9326417; PIDN:AB59751.1; PID:g326424

C;Genetics:

A;Gene: env

C;Superfamily: type E retrovirus env polyprotein

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F;1-30/Domain: signal sequence #status predicted &lt;SIG&gt;

F;31-515/Product: exterior membrane glycoprotein #status predicted &lt;EXT&gt;

F;517-861/Product: transmembrane glycoprotein #status predicted &lt;TM&gt;

F;88-136-141,145-161-165-191,202,239-246-294,300,306-337-361-391,397,402,411

F;616-621,630-642,679,755-821/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 100.0%; Score 195; DB 1; Length 861;

Best Local Similarity 100.0%; Pred. No. 2; 3e-15; Mismatches 0; Indels 0; Gaps 0;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSILHSLIESONQOKEQELLELDKWAQWNWF 36

Db 643 YTSILHSLIESONQOKEQELLELDKWAQWNWF 678

RESULT 6

VCLJ3W

env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)

N;Contains: coat protein gp120; coat protein gp41

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 09-Jul-2004

C;Accession: A24774

R;Starcich, B.A.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.S.

Cell 45, 637-648, 1986

A;Title: Identification and characterization of conserved and variable regions in the env

A;Reference number: A24774; MUID:86218077; PMID:2423250

A;Accession: A24774

A;Molecule type: DNA

A;Residues: 1-856 &lt;STA&gt;

A;Cross-references: UNIPROT:P31872; GB:K03455; GB:M38432; NID:91906382

A;Genetics:

A;Gene: env

C;Superfamily: type E retrovirus env polyprotein

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F;1-29/Domain: signal sequence #status predicted &lt;SIG&gt;

F;30-501/Product: coat protein gp120 #status predicted &lt;GP1&gt;

F;502-847/Product: coat protein gp41 #status predicted &lt;GP2&gt;

F;87-134,140,145,155,155-183,197,234-241,262-276,289,295,331,338,354,360,390,394,404,447,459,

F;305-314/Domain: signal sequence #status predicted &lt;SIG&gt;

Query Match 95.4%; Score 18; DB 1; Length 856;

Best Local Similarity 94.4%; Pred. No. 2; 7e-14; Mismatches 0; Indels 0; Gaps 0;

Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSILHSLIESONQOKEQELLELDKWAQWNWF 36

Db 638 YTSILHSLIESONQOKEQELLELDKWAQWNWF 673

RESULT 7

VCLJVL

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)

N;Alternate names: coat polyprotein

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004

C;Accession: A03974  
 R;Musing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
 Nature 313, 450-458, 1985  
 A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus  
 A;Reference number: A93355; MUID:8511157; PMID:2982104  
 A;Accession: A03974  
 A;Residues: 1-856 <MUB>  
 A;Cross-references: UNIPROT:P03376; GB:K02083; NID:9555008; PIDN:AA859873.1; PID:9328559  
 C;Genetics:  
 C;Superfamily: type E retrovirus env polyprotein  
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
 F;1-3070/domain: signal sequence #status predicted <SIG>  
 F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
 F;512-856/Product: transmembrane glycoprotein #status predicted <TM>  
 F;88-136,141,156,160,184,197,230,234,241,262,276,289,295,301,312,335,356,386,392,397,406  
 F;616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 95.4%; Score 186; DB 1; Length 856;  
 Best Local Similarity 97.1%; Pred. No. 2.7e-14; Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 638 YTSILHSLIBESONQEQNEQEBELLDKWAQWNN 35  
 RESULT 8  
 VCVJSC  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 N;Alternate names: coat polyprotein  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 A;Note: host Homo sapiens (man)  
 C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 C;Accession: B28922  
 R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
 Virology 164, 531-536, 1988  
 A;Title: Envelope sequences of two new United States HIV-1 isolates.  
 A;Reference number: A28922; MUID:88210542; PMID:3369091  
 A;Accession: B28922  
 A;Molecule type: DNA  
 A;Residues: 1-861 <GUR>  
 C;Genetics:  
 A;Gene: env  
 C;Superfamily: type B retrovirus env polyprotein  
 C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
 F;1-2970/domain: signal sequence #status predicted <SIG>  
 F;30-861/Product: env polyprotein #status predicted <PPR>  
 F;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396  
 Query Match 95.4%; Score 186; DB 1; Length 861;  
 Best Local Similarity 94.4%; Pred. No. 2.7e-14; Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 YTSILHSLIBESONQEQNEQEBELLDKWAQWNNF 36  
 QY 1 YTSILHSLIBESONQEQNEQEBELLDKWAQWNNF 36  
 Db 643 YTSILHSLIBESONQEQNEQEBELLDKWAQWNNF 678  
 RESULT 9  
 S21994  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 A;Variety: isolate 27B  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C;Accession: S21994; S70421; S21996  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 submitted to the EMBL Data Library, July 1991  
 A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determin  
 A;Reference number: S21990  
 A;Accession: S21994  
 A;Molecule type: DNA  
 A;Residues: 1-357 <ST1>  
 A;Cross-references: UNIPROT:Q78119; EMBL:Y61356; NID:960181; PIDN:CAA43624.1; PID:910671;  
 A;Molecule type: DNA

A;Residues: 1-357 <STE1>  
 A;Cross-references: UNIPROT:Q78118; EMBL:Y61355; NID:960179; PIDN:CAA43622.1; PID:960180  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr  
 A;Reference number: S70417; MUID:9214209; PMID:1736940  
 A;Accession: S70421  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>  
 A;Cross-references: EMBL:X61355; NID:960179  
 C;Superfamily: type E retrovirus env polyprotein  
 Query Match 93.8%; Score 183; DB 2; Length 357;  
 Best Local Similarity 91.7%; Pred. No. 2.4e-14; Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Db 139 YTTLYIYTTEESONQEQNEQEBELLDKWAQWNNF 36  
 QY 1 YTSILHSLIBESONQEQNEQEBELLDKWAQWNNF 174  
 RESULT 10  
 S21998  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 A;Variety: isolate 28  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C;Accession: S21998; S70425  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determin  
 A;Reference number: S21990  
 A;Accession: S21998  
 A;Molecule type: DNA  
 A;Residues: 1-357 <STE1>  
 A;Cross-references: UNIPROT:Q78120; EMBL:Y61359; NID:960182; PIDN:CAA43630.1; PID:960183  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr  
 A;Reference number: S70417; MUID:9214209; PMID:1736940  
 A;Accession: S70425  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-222, 'X', 224-358 <STE2>  
 A;Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183  
 C;Superfamily: type E retrovirus env polyprotein  
 Query Match 93.8%; Score 183; DB 2; Length 358;  
 Best Local Similarity 91.7%; Pred. No. 2.4e-14; Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Db 140 YTSILHSLIBESONQEQNEQEBELLDKWAQWNNF 175  
 RESULT 11  
 S21996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C;Accession: S70422; S21996  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr  
 A;Reference number: S70417; MUID:9214209; PMID:1736940  
 A;Accession: S70422  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-357 <ST2>  
 A;Cross-references: UNIPROT:Q78119; EMBL:Y61356; NID:960181; PIDN:CAA43624.1; PID:910671;  
 A;Experimental source: patient 27L

A;Note: submitted to the EMBL Data Library, July 1991  
 C;Superfamily: type B retrovirus env polyprotein  
 Query Match 93.3%; Score 182; DB 2; Length 357;  
 Best Local Similarity 91.7%; Pred. No. 3 1e-14; 2; Mismatches 1; Indels 0; Gaps 0;  
 Matches 33; Conservative  
 Qy 1 YVSLIHSIIESQEQNEQELLDKWA\$JWNWF 36  
 Db 139 YVGLIYTLEESQEQNEQELLDKWA\$JWNWF 174

RESULT 12  
 T09448  
 envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
 C;Accession: T09448  
 R;Pang, S.; Winter, R.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, A;Reference number: Z16673  
 A;Accession: T09448  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-847 <PAN>  
 A;Cross-references: UNIPROT:Q75760; EMBL:U63632; NID:91465777; PID:91465781  
 C;Genetics:  
 A;Gene: env  
 C;Superfamily: type B retrovirus env polyprotein  
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
 F;1-235/Product: coat protein gp120 (fragment) #status predicted <GP1>  
 F;254-445/Product: coat protein gp1 (fragment) #status predicted <GP2>  
 F;426-445/Domain: transmembrane #status predicted <TMN>  
 F;9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:  
 Query Match 91.3%; Score 178; DB 2; Length 445;  
 Best Local Similarity 88.9%; Pred. No. 1.2e-13; 4; Mismatches 0; Indels 0; Gaps 0;  
 Matches 32; Conservative  
 Qy 1 YVSLIHSIIESQEQNEQELLDKWA\$JWNWF 36  
 Db 380 YVSLIYVLEESQEQNEQELLDKWA\$JWNWF 415

RESULT 13  
 S13289  
 env protein - human immunodeficiency virus type 1  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C;Accession: S13289  
 R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
 A;Reference number: S13288; MUID:91043044; PMID:2172833  
 A;Accession: S13289  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-358 <S1E>  
 A;Cross-references: UNIPROT:Q78140; EMBL:X61351; NID:960184; PID:960185  
 C;Superfamily: type B retrovirus env polyprotein  
 Query Match 90.8%; Score 177; DB 2; Length 358;  
 Best Local Similarity 88.9%; Pred. No. 1.2e-13; 3; Mismatches 1; Indels 0; Gaps 0;  
 Matches 32; Conservative  
 Qy 1 YVSLIHSIIESQEQNEQELLDKWA\$JWNWF 36  
 Db 140 YVSLIYVLEESQEQNEQELLDKWA\$JWNWF 175

RESULT 14  
 A41621  
 env polyprotein M - human immunodeficiency virus type 1 (fragment)  
 N;Alternate names: coat polyprotein  
 N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 A;Note: host Homo sapiens (man)  
 C;Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

Search completed: September 20, 2005, 19:48:29  
 Job time: 40 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

Om protein - protein search, using sw model  
Run on: September 20, 2005, 19:24:39 ; Search time 173 Seconds  
(without alignments)  
106.560 Million cell updates/sec

Title: US-09-809-060A-1

Perfect score: 195

Sequence: 1 YTSIHLHSIIESQESNQKEQNEQELLDKWAISLWNWF 36

Scoring table: BLASTM62  
Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : UniProt 03,\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195	100.0	645	2 Q93A6	Q93A6 PRELIMINARY; PRT; 645 AA.
2	195	100.0	747	2 Q71067	Q93A6; 2001 (TREMBrel. 17, Created) DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
3	195	100.0	748	2 Q71066	DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)
4	195	100.0	752	2 Q71064	DE Truncated envelope glycoprotein (Fragment).
5	195	100.0	752	2 Q71065	GN Name=env;
6	195	100.0	752	2 Q71068	OS Human immunodeficiency virus 1.
7	195	100.0	851	1 ENV_HV1BB	OC Viruses; Retroviridae; Lentivirus.
8	195	100.0	851	2 Q78243	OX NCBI_TaxID=11676;
9	195	100.0	852	2 Q6TAP8	RN [1]
10	195	100.0	852	2 Q6TA99	SEQUENCE FROM N.A.
11	195	100.0	852	2 Q6TQ1	RX MEDLINE=21192672; PubMed=11287644; DOI=10.1073/pnas.071063898;
12	195	100.0	852	2 Q6TQ2	RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riburdy J.M.,
13	195	100.0	852	2 Q6TQ3	RA White S.W., Doherty P.C., Hurwitz J.I.;
14	195	100.0	852	2 Q6TQ4	RT "localization of CD4+ T cell epitope hotspots to exposed strands of
15	195	100.0	852	2 Q6TQ5	RT HIV envelope glycoprotein suggests structural influences on antigen
16	195	100.0	852	2 Q6TQ6	RT processing";
17	195	100.0	854	2 Q6BC06	RL Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).
18	195	100.0	854	2 Q6TAN3	RL EMBL; AP321563; RAKI1810.1; -.
19	195	100.0	854	2 Q6TAN4	DR HSSP; P20871; IC24.
20	195	100.0	854	2 Q6TAN5	DR GO; GO_0016021; C: integral to membrane; IEA.
21	195	100.0	854	2 Q6TAN6	DR GO; GO_0019028; C: viral capsid; IEA.
22	195	100.0	854	2 Q6TAN7	DR GO; GO_0019031; C: viral envelope; IEA.
23	195	100.0	854	2 Q6TAN8	DR GO; GO_0005198; P: structural molecule activity; IEA.
24	195	100.0	854	2 Q6TAN9	DR InterPro; IPR000228; Env_GP41.
25	195	100.0	854	2 Q6TAN10	DR InterPro; IPR000777; GP120.
26	195	100.0	855	1 ENV_HV1B1	DR Pfam; PP00516; GP120; 1.
27	195	100.0	856	1 ENV_HV1H2	DR Pfam; PP00517; GP41; 1.
28	195	100.0	856	1 ENV_HV1H3	DR AIDS; Coat protein; Envelope protein; Glycoprotein;
29	195	100.0	856	1 ENV_HV1LW	DR Transmembrane.
30	195	100.0	856	2 Q92877	FT NON_TER 1 1
31	195	100.0	856	2 Q74090	FT SEQUENCE 645 AA: 72485 NW; B076314BE33362EC CRC64;
					Query Match 100.0%; Score 195; DB 2; Length 645;
					Best Local Similarity 100.0%; Pred. No. 1.1e-14;
					Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
					QY 1 YTSIHLHSIIESQESNQKEQNEQELLDKWAISLWNWF 36
					Db 607 YTSIHLHSIIESQESNQKEQNEQELLDKWAISLWNWF 642
					DE Envelope glycoprotein (Fragment).
					GN Name=env;

#### ALIGNMENTS

32	195	100.0	856	2 Q74599	074599 human immun
33	195	100.0	861	1 ENV_HV1BR	P03377 human immun
34	192	98.5	853	1 ENV_HV1MP	P19551 human immun
35	191	97.9	854	2 Q9178	09178 human immun
36	191	97.9	854	2 Q78705	Q78705 human immun
37	190	97.4	856	2 Q908M7	Q908M7 human immun
38	189	96.9	616	2 Q993B0	0993b0 human immun
39	189	96.9	618	2 Q993B2	0993b2 human immun
40	189	96.9	757	2 Q9Q722	09Q722 human immun
41	189	96.9	847	2 Q7ZBZ0	Q7zbz0 human immun
42	189	96.9	848	2 Q69990	Q69990 human immun
43	187	95.9	144	2 Q7ZCB7	Q7zcb7 human immun
44	187	95.9	809	2 Q6D1T5	06G115 human immun
45	187	95.9	838	2 Q03806	Q03806 human immun

OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,  
 RT "Viral variability and serum antibody response in a laboratory worker  
 RT infected with HIV type 1 (HTLV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U12034; AAA76699.1; -.  
 DR HSSP; P04578; IAIK.  
 DR GO; GO:0019028; C:integral to membrane; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:000198; F:structural molecule activity; IEA.  
 DR InterPro; IPR00328; Env Gp41.  
 DR InterPro; IPR000777; GPI20.  
 DR Pfam; PF00516; GPI20; 1.  
 DR Pfam; PF00517; Gp41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 FT NON TER  
 SQ 1 YTSЛИHSLIRESQNQEKNEQELLEDKWA\$LNWF 36  
 Db 633 YTSЛИHSLIRESQNQEKNEQELLEDKWA\$LNWF 668

RESULT 3

Query Match 100.0%; Score 195; DB 2; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-14;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSЛИHSLIRESQNQEKNEQELLEDKWA\$LNWF 36  
 RN 747 AA; 84250 MW; 732E936A52245F14 CRC64;

Db 633 YTSЛИHSLIRESQNQEKNEQELLEDKWA\$LNWF 668

RESULT 4

Query Match 100.0%; Score 195; DB 2; Length 748;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-14;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSЛИHSLIRESQNQEKNEQELLEDKWA\$LNWF 36  
 RN 748 AA; 84224 MW; 56BBDFF186C67694B CRC64;

Db 634 YTSЛИHSLIRESQNQEKNEQELLEDKWA\$LNWF 669

RESULT 5

Query Match 100.0%; Score 195; DB 2; Length 752;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-14;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSЛИHSLIRESQNQEKNEQELLEDKWA\$LNWF 36  
 Db 634 YTSЛИHSLIRESQNQEKNEQELLEDKWA\$LNWF 673

DR Pfam; PF00516; GPI20; 1.  
 DR Pfam; PF00517; Gp41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 FT NON TER  
 SQ 1 YTSЛИHSLIRESQNQEKNEQELLEDKWA\$LNWF 36  
 DR HSSP; P04578; IAIK.  
 DR GO; GO:0019028; C:integral to membrane; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:000198; F:structural molecule activity; IEA.  
 DR InterPro; IPR00328; Env Gp41.  
 DR InterPro; IPR000777; GPI20.  
 DR Pfam; PF00516; GPI20; 1.  
 DR Pfam; PF00517; Gp41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 FT NON TER  
 SQ 1 YTSЛИHSLIRESQNQEKNEQELLEDKWA\$LNWF 36  
 DR HSSP; P04578; IAIK.  
 DR GO; GO:0019028; C:integral to membrane; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:000198; F:structural molecule activity; IEA.  
 DR InterPro; IPR00328; Env Gp41.  
 DR InterPro; IPR000777; GPI20.



RT chronically infected HTT-78 cellular clone.;"

RL J. Viral Dis. 1:40-55 (1992).

DR EMBL; Z11530; CAA7628.1; -.

DR PIR; A53591; A53591.

DR PIR; S13288; S13288.

DR PIR; S33985; S33985.

DR HSSP; P04578; IAIK.

DR GO; GO; 0016021; C: integral to membrane; IEA.

DR GO; GO; 0019028; C:viral capsid; IEA.

DR GO; GO; 0019031; C:viral envelope; IEA.

DR GO; GO; 0005198; F: structural molecule activity; IEA.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

SQ SEQUENCE 851 AA; 9629 MW; 1A37679B7E88027 CRC64;

Query Match 100.0%; Score 195; DB 1; Length 851;

Best Local Similarity 100.0%; Pred. No. 1.5e-14;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIHLISLIESQONQEKNEQELLEDKWLKASLWNWF 36

Db 633 YTSLIHLISLIESQONQEKNEQELLEDKWLKASLWNWF 668

---

RESULT 8

Q78243 PRT; 851 AA.

PRELIMINARY; PRT; 851 AA.

ID Q78243; 07/24/1996 (TREMBIrel. 01, Created)

DT 01-NOV-1996 (TREMBIrel. 01, Last sequence update)

DT 01-OCT-2003 (TREMBIrel. 25, Last annotation update)

DB Env Polyprotein.

GN Name-env;

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

OX NCBI\_TAXID=11676;

RN [1]

SEQUENCE FROM N.A.

RP Published=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;

RA Pastor C., Ramos A., Mosier D.E.;

RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching,"

RL J. Virol. 78:7565-7574 (2004).

DR EMBL; AY26109; ARX05833.1; -.

DR EMBL; AY26107; ARX05831.1; -.

DR GO; GO; 0016021; C:integral to membrane; IEA.

DR GO; GO; 0019028; C:viral capsid; IEA.

DR GO; GO; 0019031; C:viral envelope; IEA.

DR GO; GO; 0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env GP41.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

DR AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;

KW Transmembrane.

SQ SEQUENCE 852 AA; 96903 MW; 3FB7D44D8E6FBFC CRC64;

Query Match 100.0%; Score 195; DB 2; Length 852;

Best Local Similarity 100.0%; Pred. No. 1.5e-14;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIHLISLIESQONQEKNEQELLEDKWLKASLWNWF 36

Db 634 YTSLIHLISLIESQONQEKNEQELLEDKWLKASLWNWF 669

---

RESULT 10

Q6TAP9 PRELIMINARY; PRT; 852 AA.

ID Q6TAP9; 06/29/2004 (TREMBIrel. 01, Created)

DT 06/29/2004 (TREMBIrel. 01, Last sequence update)

DT 25-OCT-2004 (TREMBIrel. 28, Last annotation update)

DB Envelope glycoprotein.

GN Name-env;

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

OX NCBI\_TAXID=11676;

RN [1]

SEQUENCE FROM N.A.

RP Published=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;

RA Pastor C., Ramos A., Mosier D.E.;

RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching,"

RL J. Virol. 78:7565-7574 (2004).

DR EMBL; AY26109; ARX05833.1; -.

DR EMBL; AY26107; ARX05831.1; -.

DR GO; GO; 0016021; C:integral to membrane; IEA.

DR GO; GO; 0019028; C:viral capsid; IEA.

DR GO; GO; 0019031; C:viral envelope; IEA.

DR GO; GO; 0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env GP41.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

DR AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;

KW Transmembrane.

SQ SEQUENCE 852 AA; 96903 MW; 3FB7D44D8E6FBFC CRC64;

Query Match 100.0%; Score 195; DB 2; Length 852;

Best Local Similarity 100.0%; Pred. No. 1.5e-14;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIHLISLIESQONQEKNEQELLEDKWLKASLWNWF 36

Db 634 YTSLIHLISLIESQONQEKNEQELLEDKWLKASLWNWF 669

DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DE Envelope glycoprotein.  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;  
 RA Pastore C., Ramos A., Mosier D.E.;  
 RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching";  
 RL J. Virol. 78:7565-7574(2004).  
 DR EMBL: AY426108; AAR05832.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env GP41.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 SQ YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 36  
 Query Match 100.0%; Score 195; DB 2; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 36  
 Db 634 YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 669

RESULT 11  
 O6TAQ1 PRELIMINARY; PRT; 852 AA.  
 ID O6TAQ1  
 AC 06TAQ1  
 DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DE Envelope glycoprotein.  
 GN Name-env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;  
 RA Pastore C., Ramos A., Mosier D.E.;  
 RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching";  
 RL J. Virol. 78:7565-7574(2004).  
 DR EMBL: AY426105; AAR05829.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR InterPro; IPR000328; Env GP41.  
 DR Pfam; PF00516; GP120; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 SQ YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 852 AA; 96971 MW; 1E186A2DED50F57E CRC64;

Query Match 100.0%; Score 195; DB 2; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 36  
 Db 634 YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 669

RESULT 12  
 O6TAQ2 PRELIMINARY; PRT; 852 AA.  
 ID O6TAQ2  
 AC 06TAQ2  
 DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DE Envelope glycoprotein.  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;  
 RA Pastore C., Ramos A., Mosier D.E.;  
 RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching";  
 RL J. Virol. 78:7565-7574(2004).  
 DR EMBL: AY426105; AAR05829.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR InterPro; IPR000328; Env GP41.  
 DR Pfam; PF00516; GP120; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 SQ YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 852 AA; 96971 MW; 1E186A2DED50F57E CRC64;

Query Match 100.0%; Score 195; DB 2; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 36  
 Db 634 YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 669

RESULT 13  
 O6TAQ3 PRELIMINARY; PRT; 852 AA.  
 ID O6TAQ3  
 AC 06TAQ3  
 DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DE Envelope glycoprotein.  
 GN Name-env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;  
 RA Pastore C., Ramos A., Mosier D.E.;  
 RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching";  
 RL J. Virol. 78:7565-7574(2004).  
 DR EMBL: AY426104; AAR05828.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR InterPro; IPR000328; Env GP41.  
 DR Pfam; PF00516; GP120; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 SQ YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 852 AA; 97001 MW; 8DF59CADDAC145E CRC64;

Query Match 100.0%; Score 195; DB 2; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 36  
 Db 634 YTSЛИHSLIESQNQКНЕQБLДKWAШLWNWF 669





RESULT 2  
 US-08-486-099-1  
 Sequence 1, Application US/08486099  
 ;  
 GENERAL INFORMATION:  
 ;  
 APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Pettaway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
 TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
 TITLE OF INVENTION: B VIRUS TRANSMISSION  
 NUMBER OF SEQUENCES: 209  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/486,099  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REFERENCE/DOCKET NUMBER: 30,742  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 ;  
 US-08-486-099-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSILHSLIESQEQNEQELLEDKWAISLWWF 36  
 Db 1 YTSILHSLIESQEQNEQELLEDKWAISLWWF 36

RESULT 3  
 US-09-071-877-1  
 Sequence 1, Application US/09071877  
 ;  
 GENERAL INFORMATION:  
 ;  
 APPLICANT: Kang, Myung-Choi  
 APPLICANT: Bray, Brian  
 APPLICANT: Lichy, Maynard  
 APPLICANT: Mader, Catherine  
 APPLICANT: Merutka, Gene  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS  
 FILE REFERENCE: 7872-050

Query Match 100.0%; Score 195; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSILHSLIESQEQNEQELLEDKWAISLWWF 36

RESULT 4  
 US-08-360-107A-1  
 Sequence 1, Application US/08360107A  
 ;  
 PATENT NO. 6017536  
 GENERAL INFORMATION:  
 ;  
 APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Pettaway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
 TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
 TITLE OF INVENTION: TRANSMISSION  
 NUMBER OF SEQUENCES: 149  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/360,107A  
 FILING DATE: 20-DEC-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REFERENCE/DOCKET NUMBER: 30,742  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 ;  
 US-08-360-107A-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSILHSLIESQEQNEQELLEDKWAISLWWF 36

Db 1 ||||||| YTSILHSIIESONQEQEELDKWASLWNWF 36

RESULT 5

US-08-484-223B-1

Sequence 1, Application US/08484223B

PATENT NO. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie &amp; Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
 TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
 TITLE OF INVENTION: TRANSMISSION  
 NUMBER OF SEQUENCES: 273  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patientin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/919, 597

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/470, 896

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30, 742

REFERENCE/DOCKET NUMBER: 7872-020

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-919-597-1

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-17; DB 3; Length 36;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSILHSIIESONQEQEELDKWASLWNWF 36

D0 1 YTSILHSIIESONQEQEELDKWASLWNWF 36

1 YTSILHSIIESONQEQEELDKWASLWNWF 36

RESULT 7

US-08-475-668A-1

Sequence 1, Application US/08475668A

GENERAL INFORMATION:  
 APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 6

US-08-919-597-1

Sequence 1, Application US/08919597

PATENT NO. 605465

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.



RESULT 10  
 US-08-554-616-1  
 Sequence 1, Application US/08554616  
 Patent No. 6133418  
 GENERAL INFORMATION:  
 APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Petteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
 TITLE OF INVENTION: MEMBRANE FUSION ASSOCIATED EVENTS, INCLUDING  
 TITLE OF INVENTION: RESPIRATORY Syncytial Virus TRANSMISSION  
 NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10016

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/554,616  
 FILING DATE: 07-JUN-1993  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/073,028  
 FILING DATE: 07-JUN-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-004-999

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEX: (212) 869-8864/9741  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide

US-08-554-616-1

Query Match Best Local Similarity 100.0%; Score 195; DB 3; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide

RESULT 11  
 US-08-485-264A-1  
 Sequence 1, Application US/08485264A  
 GENERAL INFORMATION:  
 APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn  
 APPLICANT: Guthrie, Kelly  
 APPLICANT: Merutka, Gene  
 APPLICANT: Anwer, Mohamed  
 APPLICANT: Lambert, Dennis  
 TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
 TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
 FILE REFERENCE: 7872-043  
 CURRENT APPLICATION NUMBER: US/09/082,279B  
 CURRENT FILING DATE: 1998-05-20  
 NUMBER OF SEQ ID NOS: 1515  
 SEQ ID NO 15  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Core polypeptide

US-09-082-279B-15

Query Match Best Local Similarity 100.0%; Score 195; DB 3; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Core polypeptide

US-09-082-279B-36

Query Match Best Local Similarity 100.0%; Score 195; DB 3; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Core polypeptide

Db 1 YTSЛИHSLIESQNOQBNEOQBLELDKWA\$JWWF 36

RESULT 13

US-09-082-279B-497

; Sequence 497, Application US/09082279B

; Patent No. 6238782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 497

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Core polypeptide

; US-09-082-279B-497

; Query Match

; Best Local Similarity 100.0%; Score 195; DB 3; Length 36;

; Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; QY 1 YTSЛИHSLIESQNOQBNEOQBLELDKWA\$JWWF 36

; DB 1 YTSЛИHSLIESQNOQBNEOQBLELDKWA\$JWWF 36

RESULT 14

US-09-082-279B-498

; Sequence 498, Application US/09082279B

; Patent No. 6238782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

; FILE REFERENCE: 7872-043

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 498

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Core polypeptide

; US-09-082-279B-498

; Query Match

; Best Local Similarity 100.0%; Score 195; DB 3; Length 36;

; Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; QY 1 YTSЛИHSLIESQNOQBNEOQBLELDKWA\$JWWF 36

; DB 1 YTSЛИHSLIESQNOQBNEOQBLELDKWA\$JWWF 36

RESULT 15

US-09-082-279B-603

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: September 20, 2005, 19:42:06 ; Search time 168 Seconds

(without alignments)  
86.770 Million cell updates/sec

Title: US-09-809-060A-1

Perfect score: 195  
Sequence: 1 YTSLHSLIBESQNQEKNEQELLELDKWASLWNWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext: 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
> Listing first 45 summaries

Database : Published Applications AA,\*

1: /cgmn\_6/ptodata/2/pubpaa/US097\_PUBCOMB.pep:\*

2: /cgmn\_6/ptodata/2/pubpaa/PCT1\_NEW\_PUB\_PEP:\*

3: /cgmn\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

4: /cgmn\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgmn\_6/ptodata/2/pubpaa/US07\_NEW\_PUB\_PEP:\*

6: /cgmn\_6/ptodata/2/pubpaa/PUBCOMB.pep:\*

7: /cgmn\_6/ptodata/2/pubpaa/US09\_NEW\_PUB\_PEP:\*

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9: /cgmn\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

10: /cgmn\_6/ptodata/2/pubpaa/US09D\_PUBCOMB.pep:\*

11: /cgmn\_6/ptodata/2/pubpaa/US09E\_PUBCOMB.pep:\*

12: /cgmn\_6/ptodata/2/pubpaa/US09F\_PUBCOMB.pep:\*

13: /cgmn\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgmn\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgmn\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgmn\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgmn\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*

18: /cgmn\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep:\*

19: /cgmn\_6/ptodata/2/pubpaa/US11B\_PUBCOMB.pep:\*

20: /cgmn\_6/ptodata/2/pubpaa/US11C\_PUBCOMB.pep:\*

21: /cgmn\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

22: /cgmn\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Length DB ID Description

1 195 100.0 36 9 US-09-809-060-1 Sequence 1, Appli

2 195 100.0 35 9 US-09-809-060-85 Sequence 85, Appli

3 195 100.0 36 9 US-09-876-202-10 Sequence 10, Appli

4 195 100.0 36 9 US-09-960-717-2 Sequence 2, Appli

5 195 100.0 36 9 US-09-779-451-5 Sequence 5, Appli

6 195 100.0 36 9 US-09-834-628-1 Sequence 1, Appli

7 195 100.0 36 9 US-09-828-615-1 Sequence 1, Appli

8 195 100.0 36 9 US-09-854-816-1 Sequence 1, Appli

9 195 100.0 36 9 US-09-854-816-108 Sequence 10, Appli

10 195 100.0 36 9 US-09-874-475-16 Sequence 16, Appli

11 195 100.0 36 10 US-09-493-346-1 Sequence 1, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-809-060-1 ; Sequence 1, Application US/09809050

Publication No. US20020010317A1

#### GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

TITLE OF INVENTION: A Method for Generating Immunogens that Elicit

TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active

FILE REFERENCE: 1900\_0260001

CURRENT APPLICATION NUMBER: US/09/809, 060

CURRENT FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: US 60/189, 981

PRIOR FILING DATE: 2000-03-17

NUMBER OF SEQ ID NOS: 87

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 1

LENGTH: 36

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-809-060-1

Query Match 100.0%; Score 195; DB 9; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLHSLIBESQNQEKNEQELLELDKWASLWNWF 36

DB 1 YTSLHSLIBESQNQEKNEQELLELDKWASLWNWF 36

Sequence 85, Application US/09809060  
 Publication No. US2002010317A1  
 GENERAL INFORMATION:  
 APPLICANT: Wild, Carl T.  
 TITLE OF INVENTION: A Method for Generating Immunogens that Elicit Neutralizing Antibodies Against Fusion-Active Regions of HIV Envelope Proteins  
 FILE REFERENCE: 1900-026001  
 CURRENT APPLICATION NUMBER: US/09/809, 060  
 CURRENT FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: US 60/189, 981  
 PRIOR FILING DATE: 2000-03-17  
 NUMBER OF SEQ ID NOS: 87  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 85  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Human immunodeficiency virus type 1  
 US-09-809-060-85

Query Match 100.0%; Score 195; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0;

Qy	1	YTSЛИHSLIESQNQEKNEQELLELDKWAШNWF	36
Db	1	YTSЛИHSLIESQNQEKNEQELLELDKWAШNWF	36

RESULT 3  
 US-09-796-202-10  
 Sequence 10, Application US/09796202  
 ; Sequence 10, Application US/09796202  
 ; Patent No. US2002006881A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dragic, Tatjana  
 ; TITLE OF INVENTION: SURFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
 ; FILE REFERENCE: 2048/61010/JPW/SIS  
 ; CURRENT APPLICATION NUMBER: US/09/796, 202  
 ; CURRENT FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SEQ ID NO: 10  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: unknown  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (11)..(36)  
 ; OTHER INFORMATION: T-20  
 ; US-09-796-202-10

Query Match 100.0%; Score 195; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0;

Qy	1	YTSЛИHSLIESQNQEKNEQELLELDKWAШNWF	36
Db	1	YTSЛИHSLIESQNQEKNEQELLELDKWAШNWF	36

RESULT 5  
 US-09-779-451-5  
 Sequence 5, Application US/09779451  
 ; Sequence 5, Application US/09779451  
 ; Patent No. US2002009452A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wild, Carl T.  
 ; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
 ; FILE REFERENCE: 1900-030003  
 ; CURRENT APPLICATION NUMBER: US/09/779, 451  
 ; CURRENT FILING DATE: 2001-08-17  
 ; PRIOR APPLICATION NUMBER: US 60/235, 901  
 ; PRIOR FILING DATE: 2000-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/181, 543  
 ; PRIOR FILING DATE: 2000-02-10  
 ; NUMBER OF SEQ ID NOS: 77  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 5  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus type 1  
 ; US-09-779-451-5

Query Match 100.0%; Score 195; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0;

Qy	1	YTSЛИHSLIESQNQEKNEQELLELDKWAШNWF	36
Db	1	YTSЛИHSLIESQNQEKNEQELLELDKWAШNWF	36

RESULT 6  
 US-09-834-628-1  
 Sequence 1, Application US/09834628  
 ; Sequence 1, Application US/09834628  
 ; Patent No. US20020119922A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HAYNES, BARTON F.  
 ; APPLICANT: PATEL, DHARAKUMAR D.  
 ; APPLICANT: ALAM, MUNIR  
 ; APPLICANT: LIAO, HUA-XIN  
 ; TITLE OF INVENTION: IMMUNOGEN  
 ; FILE REFERENCE: 1579-539

Query Match 100.0%; Score 195; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0;

Qy	1	YTSЛИHSLIESQNQEKNEQELLELDKWAШNWF	36
Db	1	YTSЛИHSLIESQNQEKNEQELLELDKWAШNWF	36

PRIOR APPLICATION NUMBER: KR 00-65664  
 PRIORITY FILING DATE: 2000-11-06  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 OTHER INFORMATION: peptide  
 OTHER INFORMATION: DP178  
 US-09-834-628-1  
 Query Match 100.0%; Score 195; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSLIHSLIESQEQKNQEQKNEQELLDKWA\$LWNWF 36  
 Db 1 YTSLIHSLIESQEQKNQEQKNEQELLDKWA\$LWNWF 36  
 RESULT 7  
 US-09-828-615-1  
 Sequence 1, Application US/09848615  
 Publication No. US2002146415A1  
 GENERAL INFORMATION:  
 APPLICANT: Olsen, William C.  
 TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
 FILE REFERENCE: 64672  
 CURRENT APPLICATION NUMBER: US/09/828,615  
 CURRENT FILING DATE: 2001-04-06  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-828-615-1  
 Query Match 100.0%; Score 195; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSLIHSLIESQEQKNQEQKNEQELLDKWA\$LWNWF 36  
 Db 1 YTSLIHSLIESQEQKNQEQKNEQELLDKWA\$LWNWF 36  
 RESULT 8  
 US-09-854-816-1  
 Sequence 1, Application US/09854816  
 Publication No. US2002151473A1  
 GENERAL INFORMATION:  
 APPLICANT: Andrew C. Braisted  
 J. Kevin Justice  
 Robert S. McDowell  
 J. Christopher Phelan  
 Melissa A. Starovasnik  
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
 NUMBER OF SEQUENCES: 113  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/854,816  
 FILING DATE: 15-May-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/965,056  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Torchia, PhD., Timothy E.  
 REGISTRATION NUMBER: 36,700  
 REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-8674  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 108:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TOPOLY: Amino Acid  
 SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
 ;US-09-854-816-108

RESULT 10  
 Query Match 100.0%; Score 195; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Publication No. US20020108252A1  
 GENERAL INFORMATION:  
 APPLICANT: Petropoulos, Christos J.  
 APPLICANT: Pakin, Neil T.  
 APPLICANT: Whitcomb, Jeanette  
 APPLICANT: Huang, Wei  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECEPTOR  
 TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS  
 FILE REFERENCE: 2793/65166  
 CURRENT APPLICATION NUMBER: US/09/874,475  
 CURRENT FILING DATE: 2001-06-04  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 16  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Fusion Inhibitor Peptide  
 ;US-09-874-475-16

Query Match 100.0%; Score 195; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Publication No. US2003004411A1  
 GENERAL INFORMATION:  
 APPLICANT: Olsen, William C.  
 APPLICANT: Maddon, Paul J.  
 TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
 FILE REFERENCE: 64672-A  
 CURRENT APPLICATION NUMBER: US/10/116,797  
 CURRENT FILING DATE: 2002-10-15  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 ;US-10-116-797-1

RESULT 11  
 Query Match 100.0%; Score 195; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Publication No. US20030082165A1  
 GENERAL INFORMATION:  
 APPLICANT: Olson, William C.  
 APPLICANT: Maddon, Paul J.  
 TITLE OF INVENTION: Compositions and Methods for Inhibition of HTV-1  
 TITLE OF INVENTION: Infection  
 FILE REFERENCE: 61009  
 CURRENT APPLICATION NUMBER: US/09/493,346  
 CURRENT FILING DATE: 2000-01-28  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 1  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 ;US-09-493-346-1

RESULT 12  
 Query Match 100.0%; Score 195; DB 10; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Publication No. US2003004411A1  
 GENERAL INFORMATION:  
 APPLICANT: Olsen, William C.  
 APPLICANT: Maddon, Paul J.  
 TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
 FILE REFERENCE: 64672-A  
 CURRENT APPLICATION NUMBER: US/10/116,797  
 CURRENT FILING DATE: 2002-10-15  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 ;US-10-116-797-1

RESULT 13  
 Query Match 100.0%; Score 195; DB 14; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Publication No. US20030103998A1  
 GENERAL INFORMATION:  
 APPLICANT: Johnson, M. Ross  
 APPLICANT: Lambert, Dennis M.  
 TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER  
 TITLE OF INVENTION: VIRAL INFECTIONS  
 TITLE OF INVENTION: USING COMBINATORY THERAPY  
 FILE REFERENCE: 7872-036  
 CURRENT APPLICATION NUMBER: US/10/252,136  
 CURRENT FILING DATE: 2002-09-20  
 PRIOR APPLICATION NUMBER: US/08/973,952  
 PRIOR FILING DATE: 1998-05-29  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 1  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Human immunodeficiency virus  
 ;US-10-252-136-1

RESULT 14  
 Query Match 100.0%; Score 195; DB 14; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-15; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Publication No. US20030104581A1  
 ;US-10-158-742A-8  
 ;Sequence 8, Application US/10158742A  
 ;Publication No. US20030104581A1

GENERAL INFORMATION:  
 APPLICANT: Hoes, Eva  
 APPLICANT: Meier, Thomas  
 APPLICANT: Pestlin, Gabriele  
 APPLICANT: Popp, Friedrich  
 APPLICANT: Reichert, Klaus  
 APPLICANT: Schmuck, Rainer  
 APPLICANT: Schneider, Bernd  
 APPLICANT: Seidel, Christoph  
 APPLICANT: Tischer, Wilhelm

TITLE OF INVENTION: PROCESS FOR MAKING ANTIFUSOGENIC FUSION PEPTIDES THAT FORM FILE REFERENCE: 20994  
 CURRENT APPLICATION NUMBER: US/10/158,742A  
 CURRENT FILING DATE: 2002-05-30  
 PRIOR APPLICATION NUMBER: EP 01114497.9  
 PRIOR FILING DATE: 2001-06-15  
 NUMBER OF SEQ ID NOS: 20

SOFTWARE:  
 SEQ ID NO 8  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:peptide T680  
 US-10-158-742A-8

Query Match 100.0%; Score 195; DB 14; Length 36;  
 Best Local Similarity 100.0%; Prod. No. 1.5e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLJHSLIBESQEQNEQELLDKVASLWWF 36  
 Db 1 YTSLJHSLIBESQEQNEQELLDKVASLWWF 36

RESULT 15  
 US-10-323-314-10  
 Sequence 10, Application US/10323314  
 Publication No. US20030139571A1  
 GENERAL INFORMATION:  
 APPLICANT: Olson, William  
 APPLICANT: Dragic, Tatjana  
 APPLICANT: Olson, William  
 TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
 FILE REFERENCE: 2049/61010-1/JPW/MAR/DJK  
 CURRENT APPLICATION NUMBER: US/10/323,314  
 CURRENT FILING DATE: 2002-12-19  
 NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 10  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: unknown  
 FEATURE:  
 NAME/KEY: PEPTIDE  
 LOCATION: (1)..(36)  
 OTHER INFORMATION: T-20  
 US-10-323-314-10

Query Match 100.0%; Score 195; DB 14; Length 36;  
 Best Local Similarity 100.0%; Prod. No. 1.5e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLJHSLIBESQEQNEQELLDKVASLWWF 36  
 Db 1 YTSLJHSLIBESQEQNEQELLDKVASLWWF 36

Search completed: September 20, 2005, 19:52:13  
 Job time : 169 secs

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CC	alpha helix at the C-terminal end of the gp41 ectodomain, and complexes with DP-107 (corresponds to amino acids 558-595), which contains a leucine zipper motif. The peptides form a complex via non-covalent protein-protein interactions, and possess anti-viral activity. Homologues of these peptides were identified by a computer assisted peptide sequence search. The peptides inhibit transmission to uninfected cells, and can also be used as type and/or subtype specific diagnostic tools. (Updated on 25-MAR-2003 to correct PN field.)
XX	Sequence 36 AA;
Query Match	100.0%; Score 36; DB 2; Length 36;
Best Local Similarity	100.0%; Pred. No. 1.4e-28;
Matches	36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SO	Sequence 36 AA;
Query Match	100.0%; Score 36; DB 2; Length 36;
Best Local Similarity	100.0%; Pred. No. 1.4e-28;
Matches	36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 YTSLHLHLIESQSONQKNEOEELLDKWLASLWNF 36
Db	1 YTSLHLHLIESQSONQKNEOEELLDKWLASLWNF 36
RESULT 3	AAW17011
ID	AAW17011 standard; peptide; 36 AA.
XX	
AC	AAW17011;
XX	
DT	17-OCT-2003 (revised)
DT	30-JUN-1997 (first entry)
XX	
DE	HIV-1 derived peptide useful for treatment of HIV infection.
XX	
PR	HIV; SIV; human; simian immunodeficiency virus; glycoprotein 41; transmembrane; anti-viral; DP-178; DP-107; vaccine; inhibition; replication; transmission.
XX	
OS	Human immunodeficiency virus 1; LAI isolate.
OS	
PN	WO960191-A1.
XX	
PD	19-DEC-1996.
XX	
PF	06-JUN-1996; 96WC-US009499.
XX	
PR	07-JUN-1995; 95US-00481957.
XX	
PA	(TRIM-) TRIMERIS INC.
XX	
PI	Johnson RM, Lambert DM;
PI	
DR	WPI; 1997-099886/09.
XX	
PR	Compns. contg. DP-178 or DP-107 in combination with other therapeutic agent - useful for treatment of HIV infection, esp. by inhibiting replication or transmission of HIV.
XX	
PT	Claim 2; Fig 1; 84pp; English.
XX	
CC	AAW17011 represents a peptide designated DP-178, a peptide derived from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The peptide corresponds to residues 638-673 of gp41. DP-178 and its derivatives are used in combination with a therapeutic agent, e.g. a reverse transcriptase, viral protease, cytokine, glycosylation or viral mRNA processing inhibitor or a nucleoside inhibitor. The peptides work by inhibiting viral replication or inhibiting transmission. They may also be used in vaccines for protecting against HIV infection. (Updated on 17-OCT-2003 to standardise OS field)
CC	
SQ	Sequence 36 AA;
Query Match	100.0%; Score 36; DB 2; Length 36;
Best Local Similarity	100.0%; Pred. No. 1.4e-28;
Matches	36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SO	Sequence 36 AA;
Query Match	100.0%; Score 36; DB 2; Length 36;
Best Local Similarity	100.0%; Pred. No. 1.4e-28;
Matches	36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 YTSLHLHLIESQSONQKNEOEELLDKWLASLWNF 36
Db	1 YTSLHLHLIESQSONQKNEOEELLDKWLASLWNF 36
RESULT 4	AY22912
ID	AY22912 standard; peptide; 36 AA.
XX	
AC	AY22912;
XX	
DT	19-AUG-1999 (first entry)
XX	
DE	SEQ ID NO. 108 from WO9820036.

Query Match 100.0%; Score 36; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-28;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



KW T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN W09948513-A1.  
 XX  
 PD 30-SEP-1999.  
 XX  
 PR 22-MAR-1999; 99WO-US006230.  
 XX  
 PR 23-MAR-1998; 98US-00045920.  
 XX  
 PR 01-MAY-1998; 98US-00071877.  
 XX  
 PR (TRIM-) TRIMERIS INC.  
 XX  
 PT Kang M, Bray B, Lichty M, Mader C, Merutka G;  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 XX  
 PT Kang M, Bray B, Lichty M, Mader C, Merutka G;  
 XX  
 DR WPI; 1999-591038/50.  
 XX  
 PT Methods of peptide synthesis, particularly used to produce T-20 or T-20  
 PT like peptides.  
 XX  
 PS Disclosure; Page 9; 120pp; English.  
 XX  
 The present sequence represents a peptide, designated T-20 (or DP-178),  
 CC that corresponds to amino acids 638-673 of the transmembrane protein gp41  
 CC of HIV-1 LAI isolate. The invention relates to methods for the synthesis  
 CC of peptides, in particular C- and N-terminal modified T-20 (see AY31955)  
 CC and T-20-like peptides. The method involves synthesizing specific side-  
 CC chain protected peptide fragment intermediates (see AY31956-73) of T-20  
 CC or a T-20-like peptide on a solid support, coupling the protected  
 CC fragments in solution to form a protected T-20 or T-20-like peptide,  
 CC followed by deprotection of the side chains to yield the final T-20 or T-  
 CC 20-like peptide. The invention also relates to individual peptide  
 CC fragments which act as intermediates in the synthesis of peptides of  
 interest (e.g. T-20), and to particular groups of peptide fragments which  
 CC act as intermediates in the synthesis of the peptide of interest. The  
 CC method allows for the large scale, economical production of high purity  
 CC peptides. (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 36 AA;  
 Query Match 100.0%; Score 36; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-28;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLHLSLIESQNQEKNEQKELDKWASLWNWF 36  
 Db 1 YTSLHLSLIESQNQEKNEQKELDKWASLWNWF 36  
 RESULT 7  
 ID AAY31955  
 XX  
 AC AAY31955;  
 XX  
 DT 21-DEC-1999 (first entry)  
 DE Synthetic peptide T-20 (DP-178).  
 XX  
 KW T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 OS Synthetic.  
 OS Human immunodeficiency virus 1.  
 XX  
 FH Key  
 FT Modified-site 1 /note= "N-terminal acetyl"  
 FT Modified-site 36 /note= "C-terminal amide"  
 PN W09948513-A1.

---

XX  
 PD 30-SEP-1999.  
 XX  
 PR 22-MAR-1999; 99WO-US006230.  
 XX  
 PR 23-MAR-1998; 98US-00045920.  
 XX  
 PR 01-MAY-1998; 98US-00071877.  
 XX  
 PR (TRIM-) TRIMERIS INC.  
 XX  
 PT Kang M, Bray B, Lichty M, Mader C, Merutka G;  
 XX  
 DR WPI; 1999-591038/50.  
 XX  
 PT Methods of peptide synthesis, particularly used to produce T-20 or T-20  
 PT like peptides.  
 XX  
 PS Claim 1; Page 102; 120pp; English.  
 XX  
 The present sequence represents an N- and C-terminal modified peptide,  
 CC designated T-20 (or DP-178), corresponding to amino acids 638-673 of the  
 transmembrane protein gp41 of HIV-1 LAI isolate. The invention relates to  
 CC methods for the synthesis of peptides, in particular T-20 and T-20-like  
 CC peptides. The method involves synthesizing specific side-chain protected  
 CC peptide fragment intermediates of T-20 or a T-20-like peptide on a solid  
 CC support, coupling the protected fragments in solution to form a protected  
 CC T-20 or T-20-like peptide, followed by deprotection of the side chains to  
 CC yield the final T-20 or T-20-like peptide. The invention also relates to  
 CC individual peptide fragments (see AY31956-73) which act as intermediates  
 CC in the synthesis of peptides of interest (e.g. T-20), and to particular  
 CC groups of peptide fragments which act as intermediates in the synthesis  
 CC of the peptide of interest. The method allows for the large scale,  
 CC economical production of high purity peptides  
 XX  
 SQ Sequence 36 AA;  
 Query Match 100.0%; Score 36; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-28;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLHLSLIESQNQEKNEQKELDKWASLWNWF 36  
 Db 1 YTSLHLSLIESQNQEKNEQKELDKWASLWNWF 36  
 RESULT 8  
 ID AAY89999  
 AC AAY89999;  
 XX  
 DT 23-MAY-2000 (first entry)  
 DE Core polypeptide fragment T No. 1598.  
 XX  
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; STV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN W09939615-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PR 20-MAY-1999; 99WO-US011219.  
 XX  
 PR 20-MAY-1998; 98US-00082279.  
 XX  
 PR (TRIM-) TRIMERIS INC.  
 XX  
 PT Barney S, Guthrie KI, Merutka G, Arner MK, Lambert DM;

CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are biactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic  
 CC factor. The peptides of the invention can be used for inhibiting viral  
 CC infection and can be used in anti-viral and anti-fusogenic treatments.  
 CC Sequences AAY8651-Y90055 represent core polypeptide fragments that can  
 CC be used in the invention. Some sequences among those indicated also  
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
 CC

XX SQ Sequence 36 AA:

Query	Match	Score	DB	Length	Best Local Similarity	Matched	Score	DB	Length	Best Local Similarity	Matched				
QY	1	YTSVLHSLIBESQNQEKNEQELLEDKWASLWNWF	36	1	YTSVLHSLIBESQNQEKNEQELLEDKWASLWNWF	36	100	0%	36	100	0%	36			
DB				1			100.0%	0	Mismatches	1.4e-20	0	Indels	0	Gaps	0

XX RESULT 10

XX AAY89777

XX ID AAY89777 standard; peptide; 36 AA.

XX AC AAY89777;

XX DT 23-MAY-2000 (first entry)

XX DE Core polypeptide fragment T No. 1343.

XX KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1; HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon; colony stimulating factor; hormone; angiogenic factor.

XX OS Unidentified.

XX PN WO9959615-A1.

XX PR 20-MAY-1999; 99WO-US011219.

XX PR 25-NOV-1999.

XX PF 20-MAY-1998; 98US-00082279.

XX PA (TRIM-) TRIMERIS INC.

XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX DR WPI; 2000-136792/12.

XX PT A new hybrid polypeptide with enhanced pharmacokinetic properties

XX PT comprises enhancer sequence.

XX Disclosure; Page 44; 124pp; English.

CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are biactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,

CC interleukin, interferon, colony stimulating factor, hormone or angiogenic  
 CC factor. The peptides of the invention can be used for inhibiting viral  
 CC infection and can be used in anti-viral and anti-fusogenic treatments.  
 CC Sequences AY8851-Y0055 represent core polypeptide fragments that can  
 CC be used in the invention. Some sequences among those indicated also  
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
 XX sequence 36 AA;

SQ Query Match 100.0%; Score 36; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-28; Mismatches 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSЛИHSLIESONQOKNEOBELLDKWAШWWF 36  
 Db 1 YTSЛИHSLIESONQOKNEOBELLDKWAШWWF 36

RESULT 11  
 AAY8982  
 ID AAY8982 standard; peptide; 36 AA.

XX  
 AC AAY8982;  
 XX

DT 23-MAY-2000 (first entry)

XX  
 DE Core polypeptide fragment T No. 1559.

XX  
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 anti-fusogenic; differentiation factor; interleukin; interferon;  
 colony stimulating factor; hormone; angiogenic factor.

XX  
 OS Unidentified.

XX  
 PR W09959615-A1.

XX  
 PN W09959615-A1.

XX  
 PD 25-NOV-1999.

XX  
 PP 20-MAY-1999; 99WO-US011219.

XX  
 PR 20-MAY-1999; 99US-00082279.

XX  
 PA (TRIM-) TRIMERIS INC.

XX  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX  
 DR WPI; 2000-136792/12.

XX  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 comprises enhancer sequence.

XX  
 PS Disclosure; Page 36; 124pp; English.

XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any core  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic  
 CC factor. The peptides of the invention can be used for inhibiting viral  
 CC infection and can be used in anti-viral and anti-fusogenic treatments.  
 CC Sequences AAY8651-Y9055 represent core polypeptide fragments that can  
 CC be used in the invention. Some sequences among those indicated also  
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
 XX sequence 36 AA;

Qy Query Match 100.0%; Score 36; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-28; Mismatches 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSЛИHSLIESONQOKNEOBELLDKWAШWWF 36  
 Db 1 YTSЛИHSLIESONQOKNEOBELLDKWAШWWF 36

RESULT 12  
 AAY8424  
 ID AAY8424 standard; peptide; 36 AA.

XX  
 AC AAY8424;  
 XX

DT 23-MAY-2000 (first entry)

XX  
 DE Core polypeptide fragment T No. 974.

XX  
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 anti-fusogenic; differentiation factor; interleukin; interferon;  
 colony stimulating factor; hormone; angiogenic factor.

XX  
 OS Unidentified.

XX  
 PR W09959615-A1.

XX  
 PN W09959615-A1.

XX  
 PD 25-NOV-1999.

XX  
 PP 20-MAY-1999; 99WO-US011219.

XX  
 PR 20-MAY-1999; 99US-00082279.

XX  
 PA (TRIM-) TRIMERIS INC.

XX  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX  
 DR WPI; 2000-136792/12.

XX  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 comprises enhancer sequence.

XX  
 PS Disclosure; Page 36; 124pp; English.

XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any core  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic  
 CC factor. The peptides of the invention can be used for inhibiting viral  
 CC infection and can be used in anti-viral and anti-fusogenic treatments.  
 CC Sequences AAY8651-Y9055 represent core polypeptide fragments that can  
 CC be used in the invention. Some sequences among those indicated also  
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
 XX sequence 36 AA;

Qy Query Match 100.0%; Score 36; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-28; Mismatches 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSЛИHSLIESONQOKNEOBELLDKWAШWWF 36  
 Db 1 YTSЛИHSLIESONQOKNEOBELLDKWAШWWF 36



XX  
 XX 25-NOV-1993.  
 PD  
 XX  
 PP 20-MAY-1999; 99WO-US011219.  
 XX  
 PR 20-MAY-1998; 98US-00082279.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 XX  
 PT Barney S, Guthrie KR, Merutka G, Anwer MK, Lambert DM;  
 XX  
 DR WPI; 2000-13679/12.  
 XX  
 A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence.  
 XX  
 PS Disclosure; Page 48; 124pp; English.  
 XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HTV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic  
 CC factor. The peptides of the invention can be used for inhibiting viral  
 CC infection and can be used in anti-viral and anti-fusogenic treatments.  
 CC Sequences KAY8851-Y0055 represent core polypeptide fragments that can  
 CC be used in the invention. Some sequences among those indicated also  
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
 XX  
 SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-28;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	YTSILHSLIESQNKQEKNEQPKLKDQWASHWNWF	36
Db	1	YTSILHSLIESQNKQEKNEQPKLKDQWASHWNWF	36

Search completed: September 20, 2005, 19:55:06  
 Job time : 168 sec



env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10) C;Alternate names: coat polyprotein N;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004 C;Accession: A03973 R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dornberger, J.A.; Papas, T.S.; Ghayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, R. Nature 313, 277-284, 1985 A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III. A;Reference number: A93353; MUID:8511123; PMID:2578615 A;Molecule type: DNA A;Residues: 1-856 <RAT> A;Cross-references: UNIPROT:P03375; GB:ML5654; GB:K02008; GB:K02009; GB:K02010; NID:9326 C;Genetics: C;Superfamily: C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein C;Domain: Signal sequence #status predicted <SIG> F;1-30/11/Product: exterior membrane glycoprotein #status predicted <EXT> F;512-856/Product: transmembrane glycoprotein #status predicted <TMM> F;88-136,41,156-160,186-197,220,234-241,262-276,289,295,301,332,339,356,386,392,397,406 F;88-136,616-625,677,674,750,816/Binding site: carbohydrate (An) (covalent) #status predicted Query Match 100.0%; Score 36; DB 1; Length 856; Best Local Similarity 100.0%; Pred. No. 4.1e-28; Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 YTSЛИHSHLIEESONQOKNEQSLLELDKWAШLWNWF 36 Db 638 YTSЛИHSHLIEESONQOKNEQSLLELDKWAШLWNWF 673

RESULT 4

VCLJLV env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a) N;Alternate names: coat polyprotein C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004 C;Accession: A03975 R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M. Cell 40, 9-17, 1985 A;Title: Nucleotide sequence of the AIDS virus, LAV. A;Reference number: A90866; MUID:85099333; PMID:2981635 A;Accession: A03975 A;Molecule type: DNA A;Residues: 1-861 <WAT> A;Cross-references: UNIPROT:P03377; GB:K02013; NID:9326417; PIDN:AAB59751.1; PID:9326424 C;Genetics: C;Superfamily: C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein C;Domain: Signal sequence #status predicted <SIG> F;1-30/11/Product: exterior membrane glycoprotein #status predicted <EXT> F;31-516/Product: transmembrane glycoprotein #status predicted <TMM> F;517-861/Product: transmembrane glycoprotein #status predicted <TMM> F;88-136,41,146-161,165,191,202,239,246-267,281-294,300,305,337 (344-361,391,397,402,411 F;616,621,630,642,679,755,821/Binding site: carbohydrate (Aan) (covalent) #status predicted Query Match 100.0%; Score 36; DB 1; Length 861; Best Local Similarity 100.0%; Pred. No. 4.2e-28; Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 YTSЛИHSHLIEESONQOKNEQSLLELDKWAШLWNWF 36 Db 643 YTSЛИHSHLIEESONQOKNEQSLLELDKWAШLWNWF 678

RESULT 5

VCLJLV env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)

C;Species: human immunodeficiency virus type 1, HIV-1  
 A;Note: host Homo sapiens (man)  
 C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
 C;Accession: A03974  
 R;Musing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
 A;Title: Nucleic acid structure and expression of the human AIDS/Lymphadenopathy retrovirus  
 A;Reference\_number: A93355; MUID:8511157; PMID:2982104  
 A;Accession: A0374  
 A;Molecule type: DNA  
 A;Residues: 1-856 <MUE>  
 A;Cross-references: UNIPROT:P03376; GB:K02083; MUID:9555008; PIDN:AB59873.1; PID:9328559  
 C;Genetics:  
 C;Superfamily: type B retrovirus env polyprotein  
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
 F;1-30/Domain: signal sequence #statutus predicted <SIG>  
 F;31-51/Product: exterior membrane glycoprotein #statutus predicted <EXT>  
 F;512-856/Product: transmembrane glycoprotein #statutus predicted <TMM>  
 F;88-1361/141,156,160,186,197,230,234,241,262,276,289,285,301,332,339,356,386,392,397,406  
 F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #statutus predicted  
 Query Match 83.3%; Score 30; DB 1; Length 856;  
 Best Local Similarity 100.0%; Predicted 3.9e-22;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSLHLHSLIESONQEQKNEQELLDKWA 30  
 Db 638 YTSLHLHSLIESONQEQKNEQELLDKWA 667

RESULT 6

S21994 envelope protein gp120/gp41 - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1, HIV-1

C;Variety: isolate 27B

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S21994; S70421

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by the EMBL data library, July 1991

A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by the EMBL data library, July 1991

A;Reference number: S21990

A;Accession: S21994

A;Molecule type: DNA

A;Residues: 1-357 <STEL>

A;Cross-references: UNIPROT:Q78118; EMBLU:X61355; MUID:960179; PIDN:CAA43622.1; PID:9601800

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by the EMBL data library, July 1991

A;Reference number: S70421

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-140, 'X', 142-312, 'X', 314-357 <STEB2>

A;Cross-references: EMBL:X61355; MUID:960179

C;Superfamily: type B retrovirus env polyprotein

Query Match 80.6%; Score 29; DB 2; Length 357;

Best Local Similarity 100.0%; Predicted No. 1.8e-21;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LIEESQNQEQKNEQELLDKWA1LNWFE 36

Db 146 LIEESQNQEQKNEQELLDKWA1LNWFE 174

RESULT 7

S21996 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Accession: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S70422; S21996

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr  
 A;Reference number: S70417; MUID:92144209; PMID:1736940  
 A;Accession: S70422  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-357 <S12>  
 A;Cross-references: UNIPROT:Q78119; EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:910671  
 A;Experimental source: patient 27L  
 A;Note: submitted to the EMBL Data Library, July 1991  
 C;Superfamily: type E retrovirus env polyprotein

RESULT 8

Query Match 80.6%; Score 29; DB 2; Length 357;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-21; Indels 0; Gaps 0;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LIBESONQEQEKNEQELLEDKWAISLWWF 36  
 Db 146 LIBESONQEQEKNEQELLEDKWAISLWWF 174

RESULT 9

env polyprotein - human immunodeficiency virus type 1 (fragment)

N;Alternate names: coat polyprotein

N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C;Species: human immunodeficiency virus type 1, HIV-1

C;Note: host Homo sapiens (man)

C;Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: C41621

R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbt, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A;Reference number: A41621; MUID:92107924; PMID:1763038

A;Accession: C41621

A;Molecule type: DNA

A;Residues: 1-443 <BUR>

A;Cross-references: UNIPROT:Q80023; GB:MT7230; NID:9328631; PIDN:AA03792.1; PID:9555015

A;Note: this virus was isolated from the mother's sexual partner

C;Genetics:

A;Gene: env

C;Superfamily: type E retrovirus env polyprotein

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F;1-231/Product: coat protein gp120 (fragment) #status predicted <GP1>

F;252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

F;424-443/Domain: transmembrane #status predicted <TM>

F;9,23,48,78,101,107,131,137,147,153,188,203,351,356,365,377/Binding site: ca

RESULT 10

env protein - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1, HIV-1

C;Accession: S13289

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S13289

R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c

A;Reference number: S13288; MUID:91043044; PMID:2172833

A;Accession: S13289

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-847 <OBR>

A;Cross-references: UNIPROT:Q75760

C;Superfamily: type E retrovirus env polyprotein

RESULT 11

env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Accession: A24774

R;Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McHeely, P.D.; Modrow, S.; Wolf, H.; Parks, B.E.

Cell 45, 637-648, 1986

A;Title: Identification and characterization of conserved and variable regions in the env

A;Reference number: A24774; MUID:86218077; PMID:2423250

A;Accession: A24774

A;Molecule type: DNA

A;Residues: 1-856 <STA>

A;Cross-references: UNIPROT:P31872; GB:K03455; GB:M38432; NID:9106382

C;Genetics:

A;Gene: env

C;Superfamily: type E retrovirus env polyprotein

C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-29/Domain: signal sequence #status predicted <SIG>

F;30-501/Product: coat protein gp120 #status predicted <GP1>

F;502-847/Product: coat protein gp41 #status predicted <GP2>

F;87, 134, 140, 151, 155, 183, 197, 234, 241, 262, 276, 289, 295, 331, 338, 354, 360, 390, 394, 404, 447, 459,

Query Match 80.6%; Score 29; DB 1; Length 856;

Best Local Similarity 100.0%; Pred. No. 3.9e-21; Indels 0; Gaps 0;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LIBESONQEQEKNEQELLEDKWAISLWWF 36  
 Db 645 LIBESONQEQEKNEQELLEDKWAISLWWF 673

RESULT 12

env polyprotein - human immunodeficiency virus type 1 (strain JRFL)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: T09448

R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL, July 1996

A;Reference number: Z16673

A;Accession: T09448

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-847 <PAN>

A;Cross-references: UNIPROT:Q75760; EMBL:U63632; NID:91465777; PID:91465781

C;Genetics:

env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 N;Alternate names: coat polyprotein  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 A;Note: host Homo sapiens (man)  
 C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 C;Accession: B28922  
 C;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by sequence analysis of two new United States HIV-1 isolates.  
 A;Title: Envelope Sequences of two new United States HIV-1 isolates.  
 A;Reference number: A28922; MUID:88219542; PMID:3369091  
 A;Accession: B28922  
 A;Molecule type: DNA  
 A;Residues: 1-861 <GUR>  
 A;Gene: env  
 C;Superfamily: type B retrovirus env polyprotein  
 C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein  
 F;1-29/Domain: signal sequence #status predicted <SIG>  
 F;30-861/Product: env polyprotein #status predicted <PP>  
 F;30-861/Product: env polyprotein #status predicted <PP>  
 Query Match 80.6%; Score 29; DB 1; Length 861;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-21;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 LIEESONQKEKNEQELLELDKWAISLNNWF 36  
 Db 650 LIEESONQKEKNEQELLELDKWAISLNNWF 678

RESULT 13  
 VCLu2  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)  
 N;Alternate names: coat polyprotein  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 A;Note: host Homo sapiens (man)  
 C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
 C;Accession: A03976  
 R;Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-  
 Science 227, 484-492, 1985  
 A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
 A;Reference number: A04003; MUID:85090453; PMID:2578227  
 A;Accession: A03976  
 A;Molecule type: DNA  
 A;Residues: 1-855 <SAN>  
 A;Cross-references: UNIPROT:PO3378; GB:K02007; NID:9328658; PIDN:AB59882.1; PID:9328666  
 C;Genetics:  
 A;Gene: env  
 C;Superfamily: type B retrovirus env polyprotein  
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
 F;1-30/Domain: signal sequence #status predicted <SIG>  
 F;31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  
 F;510-855/Product: transmembrane glycoprotein #status predicted <TM>  
 F;87-129,140-158,184-190,200-244,265,292-298,304-334,341-358,364-388,394-400,408,445,458  
 F;610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 75.0%; Score 27; DB 1; Length 855;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-19;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 EESONQKEKNEQELLELDKWAISLNNWF 36  
 Db 646 EESONQKEKNEQELLELDKWAISLNNWF 672

RESULT 14  
 S2198  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 A;Variety: isolate 28  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C;Accession: S2198  
 C;Description: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by sequence analysis of two new United States HIV-1 isolates.  
 A;Title: Envelope Sequences of two new United States HIV-1 isolates.  
 A;Reference number: S70417; MUID:92144209; PMID:1736940  
 A;Accession: S70425  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-222, X, 224-358 <ST2>  
 A;Cross-references: EMBL:X61359; NID:60182; PIDN:CAA43630.1; PID:960183  
 C;Superfamily: type B retrovirus env polyprotein  
 Query Match 69.4%; Score 25; DB 2; Length 358;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-17;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 12 SONQKEKNEQELLELDKWAISLNNWF 36  
 Db 151 SONQKEKNEQELLELDKWAISLNNWF 175

RESULT 15  
 S2192  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C;Accession: S70424; S2192  
 R;Stauder, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 C;Species: AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by sequence analysis of two new United States HIV-1 isolates.  
 A;Reference number: S70417; MUID:92144209; PMID:1736940  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-357 <ST2>  
 A;Cross-references: UNIPROT:Q78112; EMBL:X61358; NID:960177; PIDN:CAA43628.1; PID:960178  
 A;Accession: S70424  
 A;Note: submitted to the EMBL Data Library, July 1991  
 C;Superfamily: type B retrovirus env polyprotein  
 Query Match 61.1%; Score 22; DB 2; Length 357;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-14;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 12 SONQKEKNEQELLELDKWAISLNNWF 33  
 Db 150 SONQKEKNEQELLELDKWAISLNNWF 171

Search completed: September 20, 2005, 19:58:48  
 Job time : 41 secs

OM protein - protein search, using sw model									
Run on: September 20, 2005, 19:47:51 ; Search time 169 Seconds									
Minimum DB seq length: 0 (without alignments)									10.9.082 Million cell updates/sec
Post-processing: Listing first 45 summaries									
Database : UniProt 03;*									
1: uniprot_sprot:*									
2: uniprot_trembl:*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	PRELIMINARY;	PRT;	645 AA.	ALIGNMENTS
1	36	100.0	645	2	Q93A6	093A6	DT	01-JUN-2001 (TREMBLrel. 17, Created)	
2	36	100.0	747	2	Q70607	Q93A6;	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
3	36	100.0	748	2	Q70606	Q70604	DR	Truncated envelope glycoprotein (Fragment).	
4	36	100.0	752	2	Q70604	Q70605	DR	Name-env;	
5	36	100.0	752	2	Q70605	Q70605	DR	OS Human immunodeficiency virus 1.	
6	36	100.0	752	2	Q70608	Q70608	DR	Viruses; Retroviridae; Lentivirus.	
7	36	100.0	851	1	ENV_HV1B8	ENV_HV1B8	DR	OX NCBI_TaxID=11676;	
8	36	100.0	851	2	Q78243	Q93A6	DR	RN [1]	
9	36	100.0	852	2	Q6TAP9	Q70607	DR	SEQUENCE FROM N.A.	
10	36	100.0	852	2	Q6TAP9	Q70606	DR	RX MEDLINE-21192672; PubMed=11287644; DOI=10.1073/pnas.071063898;	
11	36	100.0	852	2	Q6TAQ1	Q70604	DR	RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberdy J.M.,	
12	36	100.0	852	2	Q6TAQ2	Q70605	DR	White S.W., Doherty P.C., Ruitwijk J.J.,	
13	36	100.0	852	2	Q6TAQ3	Q70608	DR	RT "localization of CD4+ T cell epitope hotspots to exposed strands of	
14	36	100.0	852	2	Q6TAQ4	Q70607	DR	HIV envelope glycoprotein suggests structural influences on antigen	
15	36	100.0	852	2	Q6TAQ5	Q70606	DR	RT processing.";	
16	36	100.0	852	2	Q89797	Q70604	DR	Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592 (2001).	
17	36	100.0	854	2	Q6BC06	Q70605	DR	DR InterPro; IPR000328; Env GP41.	
18	36	100.0	854	2	Q6TAN3	Q70608	DR	DR InterPro; IPR000777; GP120.	
19	36	100.0	854	2	Q6TAN4	Q70608	DR	PFam; PF00516; GP120; 1.	
20	36	100.0	854	2	Q6TAN5	Q70607	DR	PFam; PF00517; GP41; 1.	
21	36	100.0	854	2	Q6TAN6	Q70606	DR	KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;	
22	36	100.0	854	2	Q6TAN7	Q70605	DR	FT Transmembrane.	
23	36	100.0	854	2	Q6TAN8	Q70604	DR	NON-TER 1	
24	36	100.0	854	2	Q72502	Q72502	DR	SEQUENCE 645 AA; 72485 MW; B076514BE93362EC CRC64;	
25	36	100.0	854	2	Q85582	Q85582	DR	Query Match 100.0%; Score 36; DB 2; Length 645;	
26	36	100.0	855	1	ENV_HV1B1	ENV_HV1B1	DR	Best Local Similarity 100.0%; Pred. No. 8.9e-28;	
27	36	100.0	856	1	ENV_HV1H2	ENV_HV1H2	DR	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
28	36	100.0	856	1	ENV_HV1H3	ENV_HV1H3	DR	QY 1 YTSLIHSIIESQNEQELLDKwaslnwfp 36	
29	36	100.0	856	1	ENV_HV1LW	ENV_HV1LW	DR	Db 607 YTSLIHSIIESQNEQELLDKwaslnwfp 642	
30	36	100.0	856	2	Q92877	Q92877	DR	DE Envelope glycoprotein (Fragment).	
31	36	100.0	856	2	Q74090	Q74090	GN Name-env;		

OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TAXID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "viral variability and serum antibody response in a laboratory worker  
 RT Infected with HIV type 1 (HTLV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U12034; AAA76699.1; -.  
 DR HSSP; P04578; IAK.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 FT NON TER 748 748 MW: 56BBDP186C67694B CRC64;  
 SQ 1 YTSILHSLIESQNKNEQELLDKWAISLWNPF 36  
 Db 634 YTSILHSLIESQNKNEQELLDKWAISLWNPF 669

RESULT 4  
 ID Q70604 PRELIMINARY; PRT; 752 AA.  
 AC 070604  
 DT 01-NOV-1995 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DR Envelope glycoprotein (Fragment).  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TAXID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95127297; PubMed 7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "viral variability and serum antibody response in a laboratory worker  
 RT Infected with HIV type 1 (HTLV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U12030; AAA76661.1; -.  
 DR HSSP; P04578; IAK.  
 DR PIR; A53591; A53591.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 FT NON TER 752 752 MW: 8830E8894013B45A CRC64;  
 SQ 1 YTSILHSLIESQNKNEQELLDKWAISLWNPF 36  
 Db 638 YTSILHSLIESQNKNEQELLDKWAISLWNPF 673

RESULT 5  
 ID Q70605 PRELIMINARY; PRT; 752 AA.  
 AC 070605  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DR Envelope glycoprotein (Fragment).





DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DE Envelope glycoprotein.  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;  
 RA Pastore C., Ramos A., Mosier D.E.;  
 RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching,"  
 RL J. Virol. 78:7565-7574 (2004).  
 DR EMBL: AY426108; AAR05832.1; -.  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0016021; C:viral capsid; IEA.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 SQ 852 AA; 96971 MW; 181862DEB50F57E CRC64;  
 Query Match 100.0%; Score 36; DB 2; Length 852;  
 Best Local Similarity 100.0%; pred. No. 1.1e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QV 1 YSLIHLHSIEESQNQERNEQELLDKWAISLWNWF 36  
 Db 634 YSLIHLHSIEESQNQERNEQELLDKWAISLWNWF 669

RESULT 11  
 O6TAQ1 PRELIMINARY; PRT; 852 AA.  
 ID O6TAQ1 PRELIMINARY; PRT; 852 AA.  
 AC O6TAQ1;  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DE Envelope glycoprotein.  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;  
 RA Pastore C., Ramos A., Mosier D.E.;  
 RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching,"  
 RL J. Virol. 78:7565-7574 (2004).  
 DR EMBL: AY426105; AAR05829.1; -.  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0016028; C:viral capsid; IEA.  
 DR GO: GO:0019031; C:viral envelope; IEA.  
 DR InterPro: IPR000777; GP120.  
 DR InterPro: IPR000777; GP120; 1.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 SQ 852 AA; 96971 MW; 181862DEB50F57E CRC64;  
 Query Match 100.0%; Score 36; DB 2; Length 852;  
 Best Local Similarity 100.0%; pred. No. 1.1e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QV 1 YSLIHLHSIEESQNQERNEQELLDKWAISLWNWF 36  
 Db 634 YSLIHLHSIEESQNQERNEQELLDKWAISLWNWF 669

RESULT 13  
 O6TAQ3 PRELIMINARY; PRT; 852 AA.  
 ID O6TAQ3 PRELIMINARY; PRT; 852 AA.  
 AC O6TAQ3;  
 DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DE Envelope glycoprotein.  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;  
 RA Pastore C., Ramos A., Mosier D.E.;  
 RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching,"  
 RL J. Virol. 78:7565-7574 (2004).  
 DR EMBL: AY426104; AAR05828.1; -.  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:019028; C:viral capsid; IEA.  
 DR GO: GO:019031; C:viral envelope; IEA.  
 DR GO: GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro: IPR00328; Env GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.

Query Match 100.0%; Score 36; DB 2; Length 852;  
 Best Local Similarity 100.0%; pred. No. 1.1e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR PFam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane;  
 SQ 852 AA; 96835 MW; 92E822A98CD93B16 CRC64;  
 Query Match 100.0%; Score 36; DB 2; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSЛИHSLIESQNQKEKNEQELLEDKWA\$JWWF 36  
 Db 634 YTSЛИHSLIESQNQKEKNEQELLEDKWA\$JWWF 669  
 RESULT 14  
 06TAQ4 PRELIMINARY; PRT; 852 AA.  
 AC 06TAQ4; HSSP; P04578; IAIK.  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Envelope glycoprotein.  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirus; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;  
 RA Pastore C., Ramos A., Mosier D. E.;  
 RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor  
 Switching", J Virol. 78:7565-7574(2004).  
 RL EMBL; AY420103; AAR05827.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR003328; Env.GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane;  
 SQ SEQUENCE 852 AA; 96860 MW; 62B201D94FC1FP7A CRC64;  
 Query Match 100.0%; Score 36; DB 2; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSЛИHSLIESQNQKEKNEQELLEDKWA\$JWWF 36  
 Db 634 YTSЛИHSLIESQNQKEKNEQELLEDKWA\$JWWF 669

RT Switching";  
 RL J. Virol. 78:7565-7574(2004).  
 DR EMBL; AY420102; AAR05826.1; -.  
 DR HSSP; P04578; IAIK.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR003328; Env.GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00517; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane;  
 SQ SEQUENCE 852 AA; 96860 MW; 62B201D94FC1FP7A CRC64;  
 Query Match 100.0%; Score 36; DB 2; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSЛИHSLIESQNQKEKNEQELLEDKWA\$JWWF 36  
 Db 634 YTSЛИHSLIESQNQKEKNEQELLEDKWA\$JWWF 669

Search completed: September 20, 2005, 19:58:01  
 Job time : 170 secs





Db 1 YTSILHSLIESENQKENEQLELDKWA\$LNWF 36

RESULT 5

Sequence 1, Application US/08484223B  
Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Langlois, Alphonse J.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 245

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/919,597

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-020

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-484-223B-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-919-597-1

Query Match

Best Local Similarity 100.0%; Score 36; DB 3; Length 36; Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSILHSLIESENQKENEQLELDKWA\$LNWF 36

Db 1 YTSILHSLIESENQKENEQLELDKWA\$LNWF 36

RESULT 6

Sequence 1, Application US/08919597

Patent No. 605265

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.

US-08-919-597-1

Sequence 1, Application US/08919597

Patent No. 605265

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.

RESULT 7

Sequence 1, Application US/08475668A

Patent No. 600065

GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #11.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/475,668A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-026  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEX: (212) 869-9741/8864  
 TELX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-475,668A-1

RESULT 8  
 US-08-485,551A-1  
 Sequence 1, Application US/08485551A  
 ; Sequence 1, Application US/08485551A  
 ; Paten No. 608973  
 ; GENERAL INFORMATION:  
 APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Peteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS TRANSMISSION  
 TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS TRANSMISSION  
 NUMBER OF SEQUENCES: 211  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Penne & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #11.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,913A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-030  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEX: (212) 869-9741/8864  
 TELX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-471,913A-1

RESULT 9  
 US-08-471-913A-1  
 Sequence 1, Application US/08471913A  
 ; Sequence 1, Application US/08471913A  
 ; General Information:  
 Patent No. 6093794  
 APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Peteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS TRANSMISSION  
 NUMBER OF SEQUENCES: 214  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Penne & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10035-2711  
 COMPUTER READABLE FORM:  
 COMPUTER TYPE: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #11.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,913A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-030  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-471-913A-1

Query Match 100.0%; Score 36; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1e-29; 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0; Topology: unknown  
 US-08-485,551A-1  
 Query Match 100.0%; Score 36; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1e-29; 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0; Topology: unknown  
 US-08-471,913A-1  
 Query Match 100.0%; Score 36; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1e-29; 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; Mismatches 0; Topology: unknown  
 US-08-471-913A-1

Qy 1 YTSLIHSLIESQNOQKNEQELLDKWDKASLWNWF 36  
 Db 1 YTSLIHSLIESQNOQKNEQELLDKWDKASLWNWF 36

RESULT 10  
 US-08-554-616-1  
 ; Sequence 1, Application US/08554616  
 ; Patent No. 6133418  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bolognesi, Dani P.  
 ; APPLICANT: Matthews, Thomas J.  
 ; APPLICANT: Wild, Carl T.  
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
 ; TITLE OF INVENTION: TRANSMISSION  
 ; NUMBER OF SEQUENCES: 74  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/554,616  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/073,028  
 ; FILING DATE: 07-JUN-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7872-004-999  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864/9741  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 36 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: Peptide  
 ; US-08-485-264A-1  
 ; Query Match 100.0%; Score 36; DB 3; Length 36;  
 ; Best Local Similarity 100.0%; Pred. No. 1e-29; 0; Mismatches 0; Indels 0; Gaps 0;  
 ; Matches 36; Conservative 0; MisMatches 0; Indels 0; Gaps 0;  
 ; QY 1 YTSILHSIISSESQNEQNEQELLEDKWSLWNWF 36  
 ; Db 1 YTSILHSIISSESQNEQNEQELLEDKWSLWNWF 36  
 ;  
 RESULT 11  
 US-08-485-264A-1  
 ; Sequence 1, Application US/08485264A  
 ; Patent No. 622893  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bolognesi, Dani P.  
 ; APPLICANT: Matthews, Thomas J.  
 ; APPLICANT: Wild, Carl T.  
 ; APPLICANT: Barney, Shawn O.  
 ; APPLICANT: Lambert, Dennis M.  
 ; APPLICANT: Petteray, Stephen R.  
 ; APPLICANT: Langlois, Alphonse J.  
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
 ; TITLE OF INVENTION: MEMBRANE FUSION ASSOCIATED EVENTS, INCLUDING  
 ; TITLE OF INVENTION: RESPIRATORY Syncytial Virus TRANSMISSION  
 ; NUMBER OF SEQUENCES: 232  
 ;  
 RESULT 11  
 US-08-485-264A-1  
 ; Sequence 1, Application US/08485264A  
 ; Patent No. 622893  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bolognesi, Dani P.  
 ; APPLICANT: Matthews, Thomas J.  
 ; APPLICANT: Wild, Carl T.  
 ; APPLICANT: Barney, Shawn O.  
 ; APPLICANT: Lambert, Dennis M.  
 ; APPLICANT: Petteray, Stephen R.  
 ; APPLICANT: Langlois, Alphonse J.  
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
 ; TITLE OF INVENTION: MEMBRANE FUSION ASSOCIATED EVENTS, INCLUDING  
 ; TITLE OF INVENTION: RESPIRATORY Syncytial Virus TRANSMISSION  
 ; NUMBER OF SEQUENCES: 232  
 ;  
 CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds LLP  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/485,264A  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7872-021  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741/8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 36 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: Peptide  
 ; US-08-485-264A-1  
 ; Query Match 100.0%; Score 36; DB 3; Length 36;  
 ; Best Local Similarity 100.0%; Pred. No. 1e-29; 0; Mismatches 0; Indels 0; Gaps 0;  
 ; Matches 36; Conservative 0; MisMatches 0; Indels 0; Gaps 0;  
 ; QY 1 YTSILHSIISSESQNEQNEQELLEDKWSLWNWF 36  
 ; Db 1 YTSILHSIISSESQNEQNEQELLEDKWSLWNWF 36  
 ;  
 RESULT 12  
 US-09-082-279B-15  
 ; Sequence 15, Application US/09082279B  
 ; Patent No. 6256782  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Barney, Shawn O.  
 ; APPLICANT: Guthrie, Kelly  
 ; APPLICANT: Merutka, Gene  
 ; APPLICANT: Mohmed, Anwer  
 ; APPLICANT: Lambert, Dennis M.  
 ; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
 ; FILE REFERENCE: 7872-043  
 ; CURRENT APPLICATION NUMBER: US/09/082,279B  
 ; NUMBER OF SEQ ID NOS: 1515  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 15  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE: Other Information: Core polypeptide  
 ; OTHER INFORMATION: Core polypeptide  
 ; US-09-082-279B-15  
 ; Query Match 100.0%; Score 36; DB 3; Length 36;  
 ; Best Local Similarity 100.0%; Pred. No. 1e-29; 0; Mismatches 0; Indels 0; Gaps 0;  
 ; Matches 36; Conservative 0; MisMatches 0; Indels 0; Gaps 0;  
 ; QY 1 YTSILHSIISSESQNEQNEQELLEDKWSLWNWF 36

Db 1 YSLIHLISLIESQONQKEQNEQELLDKWASLWNWF 36

RESULT 13

; Sequence 497, Application US/09082279B

; Patent No. 6238782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merukta, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC PROPERTIES

; FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 497

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE: OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

RESULT 14

US-09-082-279B-498

; Sequence 498, Application US/09082279B

; Patent No. 6238782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merukta, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC PROPERTIES

; FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 498

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

Query Match 100.0%; Score 36; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-29; Mismatches 0; Indels 0; Gaps 0;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSLIHLISLIESQONQKEQNEQELLDKWASLWNWF 36

Db 1 YSLIHLISLIESQONQKEQNEQELLDKWASLWNWF 36

Query Match 100.0%; Score 36; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-29; Mismatches 0; Indels 0; Gaps 0;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSLIHLISLIESQONQKEQNEQELLDKWASLWNWF 36

Db 1 YSLIHLISLIESQONQKEQNEQELLDKWASLWNWF 36

Search completed: September 20, 2005, 19:59:37

Job time : 43 Secs

Query Match 100.0%; Score 36; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-29; Mismatches 0; Indels 0; Gaps 0;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSLIHLISLIESQONQKEQNEQELLDKWASLWNWF 36

Db 1 YSLIHLISLIESQONQKEQNEQELLDKWASLWNWF 36

RESULT 15

Query Match 100.0%; Score 36; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-29; Mismatches 0; Indels 0; Gaps 0;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSLIHLISLIESQONQKEQNEQELLDKWASLWNWF 36

Db 1 YSLIHLISLIESQONQKEQNEQELLDKWASLWNWF 36

US-09-082-279B-603

GenCore version 5.1.6  
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Om protein - protein search, using sw model

Run on: September 20, 2005, 19:52:21 ; Search time 168 Seconds

(without alignments)  
86.770 Million cell updates/sec

Title: US-09-809-060A-1  
Perfect score: 36

Sequence: 1 YTSLHLHLIESQESNQEQEELDKWASLWNWF 36

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1812044 seqs, 404927589 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.\*

1: /cgmn\_6/ptodata/2/pupbaa/US07\_PUBCOMB.pep: \*  
2: /cgmn\_6/ptodata/2/pupbaa/US07\_PUBCOMB.pep: \*  
3: /cgmn\_6/ptodata/2/pupbaa/US06\_PUBCOMB.pep: \*  
4: /cgmn\_6/ptodata/2/pupbaa/US06\_PUBCOMB.pep: \*  
5: /cgmn\_6/ptodata/2/pupbaa/US07\_PUBCOMB.pep: \*  
6: /cgmn\_6/ptodata/2/pupbaa/US08\_PUBCOMB.pep: \*  
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9: /cgmn\_6/ptodata/2/pupbaa/US09\_PUBCOMB.pep: \*  
10: /cgmn\_6/ptodata/2/pupbaa/US09\_PUBCOMB.pep: \*  
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13: /cgmn\_6/ptodata/2/pupbaa/US10\_PUBCOMB.pep: \*  
14: /cgmn\_6/ptodata/2/pupbaa/US10C\_PUBCOMB.pep: \*  
15: /cgmn\_6/ptodata/2/pupbaa/US10C\_PUBCOMB.pep: \*  
16: /cgmn\_6/ptodata/2/pupbaa/US10D\_PUBCOMB.pep: \*  
17: /cgmn\_6/ptodata/2/pupbaa/US10E\_PUBCOMB.pep: \*  
18: /cgmn\_6/ptodata/2/pupbaa/US11A\_PUBCOMB.pep: \*  
19: /cgmn\_6/ptodata/2/pupbaa/US11A\_PUBCOMB.pep: \*  
20: /cgmn\_6/ptodata/2/pupbaa/US11C\_PUBCOMB.pep: \*  
21: /cgmn\_6/ptodata/2/pupbaa/US60\_PUBCOMB.pep: \*  
22: /cgmn\_6/ptodata/2/pupbaa/US60\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	36	9	US-09-809-060-1	Sequence 1, Appli
2	36	100.0	35 9 US-09-809-060-85	Sequence 85, Appli
3	36	100.0	36 9 US-09-809-060-85	Sequence 10, Appli
4	36	100.0	36 9 US-09-960-717-2	Sequence 2, Appli
5	36	100.0	36 9 US-09-779-451-5	Sequence 5, Appli
6	36	100.0	36 9 US-09-834-628-1	Sequence 6, Appli
7	36	100.0	36 9 US-09-828-615-1	Sequence 1, Appli
8	36	100.0	36 9 US-09-854-816-1	Sequence 1, Appli
9	36	100.0	36 9 US-09-854-816-108	Sequence 108, Appli
10	36	100.0	36 9 US-09-874-475-16	Sequence 16, Appli
11	36	100.0	36 10 US-09-493-346-1	Sequence 1, Appli

Query Match	Best Local Similarity	Score	DB	Length	Description
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	9	36	Sequence 1, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 1, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 8, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 10, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 7, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 15, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 497, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 498, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 603, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 630, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 631, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 649, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 705, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 834, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 1076, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 1121, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 1161, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 1469, Appli
1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 1470, Appli
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1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 1597, Appli
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1 YTSLHLHLIESQESNQEQEELDKWASLWNWF	100.0%	36	14	14	Sequence 1600, Appli

Sequence 85, Application US/09809060  
 ; Publication No. US0020010317A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wild, Carl T.  
 ; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit  
 ; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active  
 ; FILE REFERENCE: 1500.026001  
 ; CURRENT APPLICATION NUMBER: US/09/809, 060  
 ; CURRENT FILING DATE: 2001-03-15  
 ; PRIOR APPLICATION NUMBER: US 60/189, 981  
 ; PRIOR FILING DATE: 2000-03-17  
 ; NUMBER OF SEQ ID NOS: 87  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 85  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus type 1  
 ; US-09-809-060-85

Query Match 100.0%; Score 36; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-26; Mismatches 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; APPLICANT: Dragic, Tatjana  
 ; APPLICANT: Olson, William  
 ; TITLE OF INVENTION: SURFACTED CCR5 PEPTIDES FOR HIV-1 INFECTION  
 ; FILE REFERENCE: 2048/61010/JPW/SIS  
 ; CURRENT APPLICATION NUMBER: US/03/796, 202  
 ; CURRENT FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 10  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: unknown  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(36)  
 ; OTHER INFORMATION: T-20  
 ; US-09-796-202-10

RESULT 3  
 US-09-796-202-10  
 ; Sequence 10, Application US/09796202  
 ; Patent No. US2002006881A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dragic, Tatjana  
 ; APPLICANT: Olson, William  
 ; TITLE OF INVENTION: SURFACTED CCR5 PEPTIDES FOR HIV-1 INFECTION  
 ; FILE REFERENCE: 2048/61010/JPW/SIS  
 ; CURRENT APPLICATION NUMBER: US/03/796, 202  
 ; CURRENT FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 10  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: unknown  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(36)  
 ; OTHER INFORMATION: T-20  
 ; US-09-796-202-10

Query Match 100.0%; Score 36; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-26; Mismatches 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; APPLICANT: Dragic, Tatjana  
 ; APPLICANT: Olson, William  
 ; TITLE OF INVENTION: SURFACTED CCR5 PEPTIDES FOR HIV-1 INFECTION  
 ; FILE REFERENCE: 2048/61010/JPW/SIS  
 ; CURRENT APPLICATION NUMBER: US/03/796, 202  
 ; CURRENT FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 10  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: unknown  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(36)  
 ; OTHER INFORMATION: T-20  
 ; US-09-796-202-10

Query Match 100.0%; Score 36; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-26; Mismatches 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; APPLICANT: Dragic, Tatjana  
 ; APPLICANT: Olson, William  
 ; TITLE OF INVENTION: SURFACTED CCR5 PEPTIDES FOR HIV-1 INFECTION  
 ; FILE REFERENCE: 2048/61010/JPW/SIS  
 ; CURRENT APPLICATION NUMBER: US/03/796, 202  
 ; CURRENT FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 10  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: unknown  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(36)  
 ; OTHER INFORMATION: T-20  
 ; US-09-796-202-10

RESULT 4  
 US-09-960-717-2  
 ; Sequence 2, Application US/09960717  
 ; Publication No. US0020086283A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HAYNES, BARTON F.  
 ; APPLICANT: PATEL, DHARAKUMAR D.  
 ; APPLICANT: ALAM, MUNIR  
 ; APPLICANT: LIAO, HUA-KIN  
 ; TITLE OF INVENTION: IMMUNOGEN  
 ; FILE REFERENCE: 1579-539

Query Match 100.0%; Score 36; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-26; Mismatches 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; APPLICANT: HAYNES, BARTON F.  
 ; APPLICANT: PATEL, DHARAKUMAR D.  
 ; APPLICANT: ALAM, MUNIR  
 ; APPLICANT: LIAO, HUA-KIN  
 ; TITLE OF INVENTION: IMMUNOGEN  
 ; FILE REFERENCE: 1579-539

RESULT 5  
 US-09-779-451-5  
 ; Sequence 5, Application US/09779451  
 ; Patent No. US2002009452A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wild, Carl T.  
 ; APPLICANT: Allaway, Graham P.  
 ; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
 ; FILE REFERENCE: 1900.030003  
 ; CURRENT APPLICATION NUMBER: US/09/779, 451  
 ; CURRENT FILING DATE: 2001-08-17  
 ; PRIOR APPLICATION NUMBER: US 60/235, 901  
 ; PRIOR FILING DATE: 2000-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/181, 543  
 ; PRIOR FILING DATE: 2000-02-10  
 ; NUMBER OF SEQ ID NOS: 77  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 5  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus type 1  
 ; US-09-779-451-5

Query Match 100.0%; Score 36; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-26; Mismatches 0; Indels 0; Gaps 0;  
 Matches 36; Conservative 0; APPLICANT: Wild, Carl T.  
 ; APPLICANT: Allaway, Graham P.  
 ; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
 ; FILE REFERENCE: 1900.030003  
 ; CURRENT APPLICATION NUMBER: US/09/779, 451  
 ; CURRENT FILING DATE: 2001-08-17  
 ; PRIOR APPLICATION NUMBER: US 60/235, 901  
 ; PRIOR FILING DATE: 2000-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/181, 543  
 ; PRIOR FILING DATE: 2000-02-10  
 ; NUMBER OF SEQ ID NOS: 77  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 5  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus type 1  
 ; US-09-779-451-5

RESULT 6  
 US-09-834-628-1  
 ; Sequence 1, Application US/09834628  
 ; Patent No. US0020119922A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YU, YEON GYU  
 ; APPLICANT: KIM, KEY-SUN  
 ; APPLICANT: JIN, BONG-SUK  
 ; APPLICANT: PEPTIDES FOR INHIBITION OF HIV INFECTION  
 ; TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
 ; FILE REFERENCE: 05823.0198-00000  
 ; CURRENT APPLICATION NUMBER: US/09/834, 628  
 ; CURRENT FILING DATE: 2001-04-16



TELECOMMUNICATION INFORMATION: ;  
 TELEPHONE: 650/225-8674  
 TELEFAX: 650/952-3881  
 INFORMATION FOR SEQ ID NO: 108;  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: Amino Acid  
 TOPOLogy: Linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
 US-09-854-816-108

RESULT 10  
 Query Match 100.0%; Score 36; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-26;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSLILHSLEESQONQEKNEQELLDKWA\$LMWWF 36  
 Db 1 YTSLILHSLEESQONQEKNEQELLDKWA\$LMWWF 36

US-09-874-475-16  
 Sequence 16, Application US/09874475  
 Publication No. US20020182592A1

GENERAL INFORMATION:  
 APPLICANT: Petropoulos, Christos J.  
 APPLICANT: Whitcomb, Jeanette  
 APPLICANT: Huang, Wei  
 APPLICANT: Parkin, Neil T.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECEPTOR  
 TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS

FILE REFERENCE: 273/65166  
 CURRENT APPLICATION NUMBER: US/09/874,475  
 CURRENT FILING DATE: 2001-06-04  
 NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 16  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Fusion Inhibitor Peptide

US-09-874-475-16

Query Match 100.0%; Score 36; DB 9; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-26;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSLILHSLEESQONQEKNEQELLDKWA\$LMWWF 36  
 Db 1 YTSLILHSLEESQONQEKNEQELLDKWA\$LMWWF 36

RESULT 11  
 US-09-493-346-1  
 Sequence 1, Application US/09493346  
 Publication No. US20030082185A1

GENERAL INFORMATION:  
 APPLICANT: Olson, William C  
 APPLICANT: Madden, Paul J  
 TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
 TITLE OF INVENTION: Infection

FILE REFERENCE: 61009  
 CURRENT APPLICATION NUMBER: US/09/493,346  
 CURRENT FILING DATE: 2000-01-28  
 NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 1  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Artificial Sequence

US-09-493-46-1  
 OTHER INFORMATION: Description of Artificial Sequence: T20 peptide

RESULT 12  
 US-10-116-797-1  
 Sequence 1, Application US/10116797  
 Publication No. US2003004411A1

GENERAL INFORMATION:  
 APPLICANT: Olsen, William C.  
 APPLICANT: Madden, Paul J.  
 TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
 FILE REFERENCE: 64672-A  
 CURRENT APPLICATION NUMBER: US10/116,797  
 CURRENT FILING DATE: 2002-10-15  
 NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-10-116-797-1

RESULT 13  
 US-10-232-136-1  
 Sequence 1, Application US/10232136  
 Publication No. US20030103998A1

GENERAL INFORMATION:  
 APPLICANT: Johnson, M. Ross  
 APPLICANT: Lambert, Dennis M.  
 TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER  
 TITLE OF INVENTION: VIRAL INFECTIONS  
 TITLE OF INVENTION: USING COMBINATORY THERAPY  
 FILE REFERENCE: 7872-036  
 CURRENT APPLICATION NUMBER: US/10/252,136  
 CURRENT FILING DATE: 2002-09-20  
 PRIOR APPLICATION NUMBER: US/08/973,952  
 PRIOR FILING DATE: 1998-05-29  
 NUMBER OF SEQ ID NOS: 82  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 1  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Human immunodeficiency virus

US-10-232-136-1

Query Match 100.0%; Score 36; DB 14; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-26;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSLILHSLEESQONQEKNEQELLDKWA\$LMWWF 36  
 Db 1 YTSLILHSLEESQONQEKNEQELLDKWA\$LMWWF 36

RESULT 14  
 US-10-118-742A-8  
 Sequence 8, Application US/10158742A

; GENERAL INFORMATION:  
; APPLICANT: Hoess, Eva  
; APPLICANT: Meier, Thomas  
; APPLICANT: Pestlin, Gabriele  
; APPLICANT: Popp, Friedrich  
; APPLICANT: Reichert, Klaus  
; APPLICANT: Schmuck, Rainer  
; APPLICANT: Schneider, Bernd  
; APPLICANT: Seidel, Christoph  
; APPLICANT: Tischer, Wilhelm  
; TITLE OF INVENTION: PROCESS FOR MAKING ANTIFUSOGENIC FUSION PEPTIDES THAT FORM FILE REFERENCE: 20904  
; CURRENT APPLICATION NUMBER: US/10/158,742A  
; CURRENT FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: EP 01114497.9  
; PRIOR FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE:  
; SEQ ID NO 8  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence.peptide T680  
; US-10-158-742A-8

Query Match 100.0%; Score 36; DB 14; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-26;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	YTSЛИHSLIБESQNQEKNEQELLDKWAШLWWF	36
Db	1	YTSЛIHSЛIБE\$QNQEKNEQELLDKWAШLWWF	36

RESULT 15  
 US-10-323-314-10  
; Sequence 10, Application US/10323314  
; Publication No. US20030119571A1  
; GENERAL INFORMATION:  
; APPLICANT: Olson, William  
; APPLICANT: Dragic, Tatjana  
; APPLICANT: Olson, William  
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
; FILE REFERENCE: 2048/61010-1JPW/MAF/DJK  
; CURRENT APPLICATION NUMBER: US/10/323,314  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: unknown  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1). (36)  
; OTHER INFORMATION: T-20  
; US-10-323-314-10

Query Match 100.0%; Score 36; DB 14; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-26;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	YTSЛИHSLIБE\$QNQEKNEQELLDKWAШLWWF	36
Db	1	YTSЛIHSЛIБE\$QNQEKNEQELLDKWAШLWWF	36

Search completed: September 20, 2005, 20:02:32  
 Job time : 169 secs

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